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<b>(21) International Application Number:</b> PCT/US98/06955 <b>(22) International Filing Date:</b> 10 April 1998 (10.04.98) <b>(30) Priority Data:</b> 08/838,821 10 April 1997 (10.04.97) US <b>(71) Applicant:</b> GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US). <b>(72) Inventors:</b> JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Walcott Avenue, Andover, MA 01810 (US). <b>(74) Agent:</b> SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).			<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> SECRETED EXPRESSED SEQUENCE TAGS (sESTs)			
<b>(57) Abstract</b>  Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.			

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## SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

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Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

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Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

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Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted

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proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

### SUMMARY OF THE INVENTION

5       The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

15 In other embodiments, the present invention provides an isolated polynucleotide  
 consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

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 30 or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide  
 comprising a nucleotide sequence which hybridizes to a sequence selected from the group  
 consisting of:

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NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID  
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NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID  
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NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID



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 NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID  
 NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID  
 5 NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;  
 or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described  
 polynucleotides.

10

### DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the  
 Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each  
 SEQ ID NO: in the Sequence Listing.

15 Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.)  
 followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

1	BV31	18	CB302	35	BZ83	52	CD244
2	BV34	19	CB318	36	BZ87	53	CD265
20 3	BV37	20	CB321	37	CB15	54	BT217
4	BV45	21	CB96	38	CB2	55	BV278
5	BV8	22	CB98	39	CB44	56	BV280
6	BV93	23	BZ42	40	CC11	57	BV282
7	BV99	24	BZ53	41	CC182	58	BV285
25 8	CB100	25	BZ56	42	CC298	59	BV286
9	CB107	26	BZ6	43	CC310	60	BV291
10	CB110	27	BZ607	44	CC323	61	BV295
11	CB114	28	BZ61	45	CC332	62	BW389
12	CB118	29	BZ62	46	CC335	63	BX135
30 13	CB123	30	BZ641	47	CC338	64	BX141
14	CB129	31	BZ644	48	CC41	65	BX148
15	CB137	32	BZ72	49	CC52	66	BZ1
16	CB239	33	BZ74	50	CD107	67	BZ16
17	CB259	34	BZ82	51	CD205	68	BZ187

	69	BZ19	103	CE159	137	CH315	171	CC194
	70	BZ205	104	CE2	138	CH325	172	CC198
	71	BZ222	105	CE347	139	BZ568	173	CC199
	72	BZ230	106	CE36	140	BZ578	174	CC205
5	73	BZ234	107	CE40	141	BZ588	175	CC215
	74	BZ244	108	CE87	142	BZ597	176	CC253
	75	BZ269	109	CG1	143	BZ598	177	CC258
	76	BZ280	110	CG44	144	CH637	178	CC259
	77	BZ288	111	CG60	145	CH644	179	CC265
10	78	BZ304	112	CG68	146	CH699	180	CC288
	79	BZ328	113	BP202	147	CI240	181	CC95
	80	BZ331	114	BP242	148	CI247	182	CC96
	81	BP646	115	BP243	149	CJ1	183	CD311
	82	BP652	116	BZ444	150	CJ19	184	CD323
15	83	BP656	117	BZ453	151	CJ24	185	CH338
	84	BP666	118	CC233	152	CJ27	186	CH355
	85	BP667	119	CC242	153	CJ3	187	CH377
	86	BP674	120	CC247	154	CJ37	188	CH421
	87	BP695	121	CC344	155	CJ42	189	CH425
20	88	BP705	122	CC346	156	CJ44	190	CH522
	89	BP713	123	CC351	157	CJ49	191	CH541
	90	BP720	124	CC359	158	CJ50	192	CH555
	91	BP750	125	CC364	159	CJ55	193	CH558
	92	BP754	126	CC365	160	CJ6	194	CH582
25	93	BW143	127	CC374	161	CJ76	195	CH595
	94	BR307	128	CE303	162	CJ77	196	CH720
	95	BR309	129	CE328	163	CJ84	197	CH723
	96	BR312	130	CG199	164	CJ86	198	CH724
	97	BR318	131	CG209	165	CJ91	199	CH735
30	98	CB187	132	CG210	166	CC111	200	CH742
	99	CB190	133	CG350	167	CC118	201	CI126
	100	CB204	134	CG354	168	CC120	202	CI129
	101	CB213	135	CG426	169	CC126	203	CI133
	102	CE120	136	CH303	170	CC130	204	CI181

	205	CI229	239	CG160	273	CI395	307	CJ397
	206	CI25	240	CG175	274	CI407	308	CJ400
	207	CI52	241	CG176	275	CI411	309	CJ404
	208	CI84	242	CG180	276	CI437	310	CJ415
5	209	CI91	243	CG279	277	CI443	311	CJ420
	210	BP163	244	CG292	278	CI444	312	CJ424
	211	BP175	245	CG300	279	CI459	313	CJ434
	212	BP199	246	CG301	280	CI480	314	CJ454
	213	BP272	247	CG314	281	CI490	315	CJ457
10	214	BP284	248	CG315	282	CI492	316	CJ481
	215	BP294	249	CG324	283	CI493	317	CJ493
	216	BP299	250	CG336	284	CI510	318	CJ501
	217	BP300	251	CG99	285	CI522	319	CJ514
	218	BP306	252	CH143	286	CI534	320	CJ539
15	219	BP311	253	CH207	287	CI542	321	CJ540
	220	BP312	254	CH224	288	CI560	322	CJ549
	221	BP327	255	CH227	289	CI561	323	CJ551
	222	BP345	256	CH245	290	CI583	324	CK126
	223	BP368	257	CH246	291	CI586	325	CK151
20	224	BP467	258	CH27	292	CJ145	326	CK181
	225	BP468	259	CH30	293	CJ149	327	CK201
	226	BR375	260	CH4	294	CJ160	328	CK213
	227	BR390	261	CH64	295	CJ164	329	CK218
	228	BR408	262	CH78	296	CJ168	330	CK234
25	229	BR418	263	CH85	297	CJ176	331	CK37
	230	BY66	264	CH87	298	CJ183	332	CK48
	231	CF118	265	CN320	299	CJ194	333	CL104
	232	CF127	266	CN343	300	CJ206	334	CL110
	233	CF22	267	CN344	301	CJ230	335	CL122
30	234	CF235	268	CN395	302	CJ237	336	CL132
	235	CG109	269	CN423	303	CJ257	337	CL147
	236	CG131	270	CI363	304	CJ265	338	CL152
	237	CG153	271	CI386	305	CJ378	339	CL181
	238	CG158	272	CI392	306	CJ389	340	CL182

	341	CL399	375	CN516	409	CO58	443	CO155
	342	CL469	376	CN532	410	CO48	444	CO153
	343	CL470	377	CN552	411	CO444	445	CO145
	344	CL481	378	CN593	412	CO431	446	CO140
5	345	CL493	379	CN619	413	CO391	447	CO139
	346	CM12	380	CN621	414	CO384	448	CO128
	347	CM178	381	CN667	415	CO36	449	CO1254
	348	CM188	382	CN703	416	CO351	450	CO1247
	349	CM194	383	CN718	417	CO337	451	CO1232
10	350	CM246	384	CN729	418	CO327	452	CO1224
	351	CM251	385	CN835	419	CO315	453	CO1223
	352	CM54	386	CN896	420	CO304	454	CO1206
	353	CM62	387	CO933	421	CO270	455	CO1198
	354	CN140	388	CO924	422	CO268	456	CO1196
15	355	CN171	389	CO908	423	CO264	457	CO1194
	356	CN173	390	CO900	424	CO261	458	CO1187
	357	CN238	391	CO889	425	CO257	459	CO1180
	358	CN29	392	CO888	426	CO253	460	CO1178
	359	CN291	393	CO874	427	CO25	461	CO1175
20	360	CN304	394	CO851	428	CO246	462	CO117
	361	CN327	395	CO83	429	CO244	463	CO1168
	362	CN49	396	CO821	430	CO240	464	CO1164
	363	CN50	397	CO806	431	CO228	465	CO1162
	364	CN54	398	CO798	432	CO223	466	CO1161
25	365	CN65	399	CO79	433	CO222	467	CO1159
	366	CJ305	400	CO71	434	CO209	468	CO1153
	367	CJ316	401	CO7	435	CO205	469	CO1151
	368	CJ317	402	CO69	436	CO204	470	CO1137
	369	CJ336	403	CO66	437	CO20	471	CO1123
30	370	CJ347	404	CO639	438	CO197	472	CO1076
	371	CJ360	405	CO638	439	CO185	473	CO1072
	372	CJ365	406	CO625	440	CO170	474	CO1026
	373	CJ366	407	CO62	441	CO17	475	CO1000
	374	CN483	408	CO602	442	CO163	476	CN755

	477	CN736	511	CR1166	545	CR632	579	CO409
	478	CN709	512	CR1186	546	CR641	580	CO474
	479	CO975	513	CR1190	547	CT729	581	CO480
	480	CO990	514	CR329	548	CN922	582	CO500
5	481	CP280	515	CR354	549	CN934	583	CO519
	482	CP283	516	CR377	550	CN951	584	CO522
	483	CP287	517	CR390	551	CN952	585	CO526
	484	CP289	518	CR392	552	CN980	586	CO559
	485	CP294	519	CR422	553	CP111	587	CO595
10	486	CP304	520	CR423	554	CP147	588	CO605
	487	CP307	521	CR466	555	CU13	589	CO618
	488	CP311	522	CR477	556	CP251	590	CO629
	489	CP313	523	CR478	557	CP258	591	CO643
	490	CP314	524	CR482	558	CP33	592	CO653
15	491	CP328	525	CR491	559	CP41	593	CO661
	492	CP352	526	CR494	560	CP91	594	CO667
	493	CQ286	527	CR502	561	CP92	595	CO695
	494	CQ294	528	CR506	562	CQ160	596	CO696
	495	CQ304	529	CR513	563	CQ165	597	CO707
20	496	CQ309	530	CR514	564	CQ268	598	CO716
	497	CQ331	531	CR515	565	CQ30	599	CO718
	498	CQ333	532	CR527	566	CR100	600	CO720
	499	CR1116	533	CR529	567	CR178	601	CO722
	500	CR1118	534	CR537	568	CR184	602	CO736
25	501	CR1121	535	CR538	569	CR263	603	CO763
	502	CR1127	536	CR540	570	CR335	604	CO767
	503	CR1135	537	CR541	571	CR4	605	CP116
	504	CR1141	538	CR545	572	CR61	606	CP151
	505	CR1142	539	CR587	573	CR93	607	CI293
30	506	CR1144	540	CR588	574	CO282	608	CI294
	507	CR1147	541	CR593	575	CO310	609	CI298
	508	CR1155	542	CR594	576	CO334	610	CU14
	509	CR1156	543	CR611	577	CO387	611	CU2
	510	CR1162	544	CR618	578	CO390	612	CU25

	613	CU32	647	CR678	681	CT748	715	CS520
	614	CU39	648	CR726	682	CT738	716	CS524
	615	CU40	649	CR733	683	CT726	717	CS534
	616	DA10	650	CR778	684	CT706	718	CT14
5	617	DA136	651	CR836	685	CT705	719	CT142
	618	DA155	652	CR839	686	CT702	720	CT143
	619	DA16	653	CR872	687	CT693	721	CT149
	620	DA165	654	CR890	688	CT677	722	CT156
	621	DA170	655	CR916	689	CT658	723	CT159
10	622	DA183	656	CR929	690	CT645	724	CT162
	623	DA223	657	CR930	691	CT636	725	CT188
	624	DA224	658	CR936	692	CT631	726	CT189
	625	DA225	659	CR974	693	CT616	727	CT190
	626	DA227	660	CT747	694	CT611	728	CT193
15	627	DA228	661	CT727	695	CT600	729	CT194
	628	DA234	662	CT690	696	CT585	730	CT2
	629	DA244	663	CT649	697	CT583	731	CT207
	630	DA246	664	CT624	698	CS224	732	CT220
	631	DA274	665	CT564	699	CS255	733	CT223
20	632	DA471	666	CT88	700	CS267	734	CT226
	633	DA490	667	CT864	701	CS271	735	CT227
	634	DA495	668	CT857	702	CS278	736	CT24
	635	DA496	669	CT852	703	CS284	737	CT254
	636	DA504	670	CT838	704	CS296	738	CT256
25	637	DA505	671	CT808	705	CS297	739	CT258
	638	DA507	672	CT807	706	CS317	740	CT271
	639	DA516	673	CT797	707	CS319	741	CT275
	640	DA529	674	CT791	708	CS322	742	CT28
	641	DA84	675	CT785	709	CS353	743	CT284
30	642	CR1003	676	CT783	710	CS366	744	CT293
	643	CR1013	677	CT780	711	CS471	745	CO1020
	644	CR1044	678	CT771	712	CS475	746	CO1043
	645	CR1056	679	CT754	713	CS485	747	CO1067
	646	CR1063	680	CT750	714	CS516	748	CO1069

	749	CO1080	783	DB257	817	CW1617	851	CT384
	750	CO1081	784	DB343	818	CW1632	852	CT392
	751	CO1094	785	DB415	819	CW1636	853	CT394
	752	CO956	786	DB53	820	CW1640	854	CT415
5	753	CO973	787	DB85	821	CW169	855	CT421
	754	CJ471	788	CW1000	822	CW172	856	CT423
	755	CJ472	789	CW1038	823	CW173	857	CT434
	756	CJ475	790	CW1087	824	CW175	858	CT440
	757	CJ483	791	CW1100	825	CV123	859	CT443
10	758	CJ484	792	CW1109	826	CV156	860	CT450
	759	CJ485	793	CW1112	827	CV160	861	CT453
	760	CJ486	794	CW1115	828	CV192	862	CT457
	761	CJ488	795	CW1150	829	CV203	863	CT466
	762	CJ496	796	CW1155	830	CV215	864	CT474
15	763	CJ497	797	CW1177	831	CV227	865	CT475
	764	CJ498	798	CW1195	832	CV263	866	CT479
	765	CJ507	799	CW1200	833	CV275	867	CT489
	766	CJ508	800	CW1201	834	CV305	868	CT51
	767	CJ519	801	CW1214	835	CV328	869	CT519
20	768	CJ520	802	CW1225	836	CV380	870	CT521
	769	CJ521	803	CW1230	837	CV394	871	CT526
	770	CJ522	804	CW1233	838	CV410	872	CT536
	771	CJ534	805	CW1272	839	CV416	873	CT541
	772	CJ536	806	CW1292	840	CV461	874	CT547
25	773	CJ543	807	CW1306	841	CV493	875	CT550
	774	CJ544	808	CW1311	842	CV501	876	CT559
	775	CJ547	809	CW1314	843	CT3	877	CT562
	776	CK53	810	CW1334	844	CT314	878	DE36
	777	CK7	811	CW1365	845	CT317	879	DE37
30	778	CK70	812	CW1372	846	CT320	880	DE4
	779	CL49	813	CW149	847	CT326	881	DE42
	780	CL63	814	CW152	848	CT340	882	DE63
	781	DB203	815	CW1574	849	CT353	883	DE70
	782	DB208	816	CW1611	850	CT358	884	DE83

	885	DE103	919	CS771	953	CW775	987	DA337
	886	DE105	920	CS773	954	CW795	988	DA348
	887	DE110	921	CS776	955	CW802	989	DA373
	888	DE114	922	CW222	956	CW823	990	DA388
5	889	DE117	923	CW224	957	CW835	991	DA389
	890	DE119	924	CW226	958	CZ115	992	DA390
	891	DE91	925	CW232	959	CZ122	993	DA391
	892	DE95	926	CW254	960	CZ186	994	DA414
	893	DE96	927	CW272	961	CZ214	995	DA428
10	894	CW420	928	CW280	962	CZ247	996	DA443
	895	CW424	929	CW313	963	CZ251	997	DA451
	896	CW457	930	CW314	964	CZ268	998	CW1458
	897	CW485	931	CW347	965	CZ270	999	CW1475
	898	CS383	932	CW354	966	CZ278	1000	CW1481
15	899	CS384	933	CW363	967	CZ291	1001	CW1506
	900	CS399	934	CW374	968	CZ320	1002	CW1510
	901	CS405	935	CW382	969	CZ326	1003	CW1543
	902	CS409	936	CW383	970	CZ362	1004	CW1550
	903	CS431	937	CW386	971	CW1414	1005	CW1552
20	904	CS438	938	CW388	972	CW1440	1006	CZ372
	905	CS454	939	CW512	973	CE209	1007	CZ374
	906	CS588	940	CW517	974	CE216	1008	CW902
	907	CS629	941	CW53	975	CE232	1009	CW922
	908	CS636	942	CW554	976	CE242	1010	CW924
25	909	CS637	943	CW585	977	CF193	1011	CW976
	910	CS638	944	CW618	978	CH776	1012	CW979
	911	CS645	945	CE197	979	CW1381	1013	CW984
	912	CS679	946	CW662	980	CW1389	1014	CW998
	913	CS682	947	CW675	981	CW1399	1015	CZ1
30	914	CS734	948	CW691	982	CZ653	1016	CW753
	915	CS743	949	CW707	983	CZ681	1017	CW759
	916	CS752	950	CW735	984	CZ711	1018	CW800
	917	CS756	951	CW762	985	CZ719	1019	CW891
	918	CS765	952	CW768	986	DA306	1020	CW960



	1021	CT80	1055	DC14	1089	DH1206	1123	DF478
	1022	DF1115	1056	CW1670	1090	DH1212	1124	DF483
	1023	DF1117	1057	CW1682	1091	DH1213	1125	DF494
	1024	DF1125	1058	DF814	1092	DH190	1126	DF499
5	1025	DF134	1059	DF821	1093	DI191	1127	DF7
	1026	DF14	1060	DF842	1094	DI207	1128	DF706
	1027	DF163	1061	DG1	1095	DI216	1129	DF713
	1028	DF174	1062	DG17	1096	DI243	1130	DF727
	1029	DF175	1063	DG174	1097	DI248	1131	DF737
10	1030	DF180	1064	DG256	1098	DI261	1132	DF756
	1031	DF185	1065	DG26	1099	DF1005	1133	DF757
	1032	DF201	1066	DG266	1100	DF1009	1134	DF762
	1033	DF202	1067	DG326	1101	DF1010	1135	DF776
	1034	DF203	1068	DG327	1102	DF102	1136	DF777
15	1035	DF206	1069	DG329	1103	DF1050	1137	DF780
	1036	DF219	1070	DG330	1104	DF1062	1138	DF783
	1037	DF230	1071	DG331	1105	DF1063	1139	DG12
	1038	DF232	1072	DG44	1106	DF1084	1140	DG121
	1039	DF239	1073	DG65	1107	DF153	1141	DG128
20	1040	DF244	1074	DG69	1108	DF218	1142	DG141
	1041	DF259	1075	DG7	1109	DF251	1143	DG149
	1042	DF266	1076	DG71	1110	DF280	1144	DH28
	1043	DF46	1077	DG76	1111	DF286	1145	DH303
	1044	DF65	1078	DG82	1112	DF316	1146	DH318
25	1045	DF69	1079	DH1086	1113	DF317	1147	DH322
	1046	DB145	1080	DH1098	1114	DF343	1148	DH340
	1047	DB150	1081	DH1135	1115	DF347	1149	DH371
	1048	DB159	1082	DH1145	1116	DF370	1150	DH40
	1049	DB174	1083	DH1153	1117	DF382	1151	DH401
30	1050	DB180	1084	DH1182	1118	DF396	1152	DH432
	1051	CY1	1085	DH1185	1119	DF428	1153	DH451
	1052	CY11	1086	DH1190	1120	DF453	1154	DH496
	1053	CY3	1087	DH1191	1121	DF457	1155	DH502
	1054	CY9	1088	DH1201	1122	DF460	1156	DH529

	1157	DH66	1191	DF915	1225	DH1357	1259	DI501
	1158	DF518	1192	DF948	1226	DH145	1260	DI504
	1159	DF521	1193	DF950	1227	DH999	1261	DK111
	1160	DF538	1194	DF956	1228	DI160	1262	DK113
5	1161	DF543	1195	DF966	1229	DI386	1263	DK120
	1162	DF545	1196	DF968	1230	DI391	1264	DK122
	1163	DF547	1197	DF971	1231	DI435	1265	DK126
	1164	DF568	1198	DF973	1232	DI448	1266	DK134
	1165	DF587	1199	DF979	1233	DI454	1267	DK136
10	1166	DF589	1200	DF984	1234	DJ109	1268	DK150
	1167	DF591	1201	DF989	1235	DJ146	1269	DK160
	1168	DF601	1202	DH1257	1236	DJ167	1270	DK170
	1169	DF606	1203	DH1308	1237	DF1065	1271	DK182
	1170	DF62	1204	DH1314	1238	DI387	1272	DK185
15	1171	DF620	1205	DI341	1239	DI393	1273	DK197
	1172	DF625	1206	DH1265	1240	DI403	1274	DK206
	1173	DF648	1207	DI349	1241	DI430	1275	DK219
	1174	DF657	1208	DI355	1242	DI438	1276	DK223
	1175	DF659	1209	DI362	1243	DJ2	1277	DK227
20	1176	DF661	1210	DI366	1244	DJ188	1278	DK229
	1177	DF662	1211	DI508	1245	DJ238	1279	DK230
	1178	DF670	1212	DI516	1246	DJ259	1280	DK243
	1179	DF674	1213	DI518	1247	DK64	1281	DK264
	1180	DF682	1214	DF1066	1248	DK70	1282	DK268
25	1181	DF688	1215	DF1069	1249	DK81	1283	DK31
	1182	DF810	1216	DG279	1250	DK84	1284	DK39
	1183	DF823	1217	DH1010	1251	DI462	1285	DK93
	1184	DF835	1218	DH1013	1252	DI466	1286	DL101
	1185	DF860	1219	DH1044	1253	DI474	1287	DL110
30	1186	DF877	1220	DH1045	1254	DI475	1288	DL116
	1187	DF883	1221	DH1073	1255	DI479	1289	DL132
	1188	DF895	1222	DH1078	1256	DI480	1290	DL63
	1189	DF909	1223	DH1340	1257	DI482	1291	DL82
	1190	DF910	1224	DH1349	1258	DI500	1292	DL95

	1293	DL99	1327	DL491	1361	DL547	1395	DO181
	1294	DJ332	1328	DL495	1362	DL550	1396	DO419
	1295	DJ362	1329	DL498	1363	DL551	1397	DO424
	1296	DK290	1330	DL504	1364	DL601	1398	DO440
5	1297	DK321	1331	DM118	1365	DL604	1399	DO447
	1298	DK324	1332	DM122	1366	DL605	1400	DO568
	1299	DK329	1333	DM126	1367	DL607	1401	DO575
	1300	DK357	1334	DM128	1368	DL608	1402	DO589
	1301	DK360	1335	DM130	1369	DL616	1403	DO610
10	1302	DL141	1336	DM147	1370	DL619	1404	DO715
	1303	DL146	1337	DM169	1371	DL620	1405	DO722
	1304	DL162	1338	DM26	1372	DL634	1406	DO737
	1305	DL163	1339	DM404	1373	DM194	1407	DO742
	1306	DL169	1340	DM406	1374	DM197	1408	DO755
15	1307	DL181	1341	DM407	1375	DM221	1409	DO765
	1308	DL185	1342	DM420	1376	DM248	1410	DO797
	1309	DL218	1343	DM425	1377	DM250	1411	DO836
	1310	DL220	1344	DM435	1378	DM262	1412	DO884
	1311	DL248	1345	DM445	1379	DM265	1413	DO896
20	1312	DL289	1346	DM449	1380	DM272	1414	CZ549
	1313	DL290	1347	DM459	1381	DM278	1415	CZ598
	1314	DL291	1348	DM462	1382	DM293	1416	DT431
	1315	DL316	1349	DM469	1383	DM303	1417	DT443
	1316	DL320	1350	DM482	1384	DM340	1418	DT446
25	1317	DL321	1351	DM6	1385	DM360	1419	DT449
	1318	DL425	1352	DM94	1386	DM365	1420	DT450
	1319	DL426	1353	DJ279	1387	DM522	1421	DT455
	1320	DL427	1354	DJ284	1388	DM533	1422	DT458
	1321	DL439	1355	DJ299	1389	DM542	1423	DN106
30	1322	DL440	1356	DJ319	1390	DM87	1424	DN153
	1323	DL444	1357	DJ323	1391	DN124	1425	DN176
	1324	DL457	1358	DL531	1392	DN144	1426	DT530
	1325	DL463	1359	DL535	1393	DN147	1427	DT534
	1326	DL466	1360	DL543	1394	DN167	1428	DT535

	1429	DT544	1463	DW1	1497	BK5
	1430	DT563	1464	DW389	1498	BK504
	1431	DT584	1465	DW398	1499	BK513
	1432	DT590	1466	DW654	1500	BK517
5	1433	DT596	1467	DW659		
	1434	DT597	1468	DW665		
	1435	DT598	1469	DW694		
	1436	DT640	1470	DW705		
	1437	DT655	1471	DW716		
10	1438	DT674	1472	DW749		
	1439	DT719	1473	DW761		
	1440	DT734	1474	DW765		
	1441	DT779	1475	DW771		
	1442	DT801	1476	DW78		
15	1443	DT802	1477	DW780		
	1444	DN696	1478	BK10		
	1445	DN697	1479	BK11		
	1446	DN704	1480	BK2		
	1447	DN710	1481	BK368		
20	1448	DN711	1482	BK373		
	1449	DN714	1483	BK374		
	1450	DN721	1484	BK375		
	1451	DN722	1485	BK384		
	1452	DN732	1486	BK402		
25	1453	DN740	1487	BK410		
	1454	DN746	1488	BK415		
	1455	DN747	1489	BK425		
	1456	DN753	1490	BK427		
	1457	DN756	1491	BK436		
30	1458	DN764	1492	BK445		
	1459	DN770	1493	BK455		
	1460	DN772	1494	BK458		
	1461	DN1120	1495	BK494		
	1462	DU372	1496	BK498		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification  
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that  
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making  
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the  
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,  
25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>‡</sup>	Wash Temperature and Buffer <sup>‡</sup>
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	< 50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	< 50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
15	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log [Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. ~~The isolated~~ polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control



sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

5 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

10 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any  
15 bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

20 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art,  
25 as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting  
30 expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl or Cibacrom blue 3GA

Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

### USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention  
5 may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

#### Research Uses and Utilities

10 The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or  
15 which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding  
20 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related  
25 DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-  
30 DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

- and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -
- 5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.
- 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune
- 20 suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may
- 25 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course,
- 30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other  
5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune  
10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from  
15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing  
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys  
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the  
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-



blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient  
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding  
10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably  
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor  
20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection  
25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or  
30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected  
5 with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured  
10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-  
15 3.19; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa  
20 et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnoli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching  
25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

30 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet  
5 transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post  
10 irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al.,  
20 *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic*  
25 *Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994;  
30 Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

#### Tissue Growth Activity

5           A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

          A protein of the present invention, which induces cartilage and/or bone growth in  
10       circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone  
15       formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

          A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of  
20       progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

          Another category of tissue regeneration activity that may be attributable to the  
25       protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein  
30       may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured  
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,  
20 alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may  
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale



et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

5           A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide  
10   particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

          A protein or peptide has chemotactic activity for a particular cell population if it can  
15   stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20           The activity of a protein of the invention may, among other means, be measured by the following methods:

          Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one  
25   cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et  
30   al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A  
5 protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors  
20 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.  
25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those  
30 described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborget al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or  
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,  
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Tumor Inhibition Activity

20 In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor  
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

30 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

20

### **ADMINISTRATION AND DOSING**

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a  
5 composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the  
10 invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or  
15 use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects  
20 of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric  
25 or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T  
30 lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5           The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, 10 diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15           As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a 25 mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous  
5 administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an  
10 adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain  
15 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical  
20 composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers,  
25 antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1 ng to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a



pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also  
5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and  
10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices  
15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as  
20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1 or 2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	Peripheral Blood Mononuclear Cell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	Salivary Gland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	Peripheral Blood Mononuclear Cell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth  
McCoy, John  
LaVallie, Edward  
Racie, Lisa  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy Disk
  - (B) COMPUTER: IBM PC Compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brown, Scott A.
  - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8224
  - (B) TELEFAX: (617) 876-5851

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 320 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

GAATTCGGCC TTCATGGCCT AAGTGTTTAA ATTATAAGCT GGTGAAGTGA AATAACACAA      60
ATCAAGCTCA CCAATTTTAA TACTCAGCTG TTGATAAACA ACACTGAAGA GTGACATTTA      120
AATTGAATT ATCTTCTTGG AAGTAGCATT GCAGCACTTT TGAATGACTT CCAAAAGGCT      180
GATCATAAAA ATCACTTCAA TCATTTTCAA ATTTTACTTT AGCAGCAATG AAGTTATTTG      240

```

GTATGACTCA GATGAACCTT CTGCTCTGTC TTGGAGTTAT TATGGTCATT TCATTTTCTG 300  
CAACCTGGGA AAACCTCGAG 320

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCC TTCATGGCCT ACGAGTGGAT CTGGTTGAGA GGAAAGCAGC TAAAAATACA 60  
GGAGATGAAA GGGATCATAA CGAACATAAT GAACCATGTT CATTATGGTT CGTGGGGAGG 120  
CAGGAAAGCA CAGTATCCAG GGCATAGGCA GAAGAGCTGT CTTTCACGGG AGGAGGGGAA 180  
CATATTCTAC TGCAATAAGC AAGGGCGGGG TAAGTACGGA TCGGGTACTT TGGGAACTAT 240  
GACGGTAGGG AGTTCAGGAA GTTGCTGCCT GAAGGCATAA AGGTTTTTTT TTTTTTTTTT 300  
TTTTTTTGCC AATTGGTCCA GTACCTCCT TCTGTGGCCC CCATCTCCAG TCTCGAG 357

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCTTA TATAATTGG ATACCTACTC ATTGTCAGTT GTATGCITTG CAAATATCTT 60  
TCCTGACCCT TACTTACCTT TCACTCTTA ATGGTATCTT TGATGAATCA AAAATTTTTC 120  
TTTTTTTGTT GTTTTTTGAG ACAGAGTCTT AACTCTGTCA CCCAGGCTGG AGTGCACTGC 180  
ATGAACATGG CTCACTGCAG CCTCAACTTC TTGGACTCAA GCAATCCTCC TGCCTCAGAA 240  
CCTCTCGAG 249

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAGCTCCTT TCCTTCTACT CTCCTGCTCA 60  
GACCATTAGT AGGTACTTTG TTAAATAAAA AACTAGATTA ACATCAATAT TACTCCAATT 120  
TGGTATCTTT TACACTATGT ATTATACCTA CTTTCTTTT ATTTCATTIA CAAATAGTTT 180  
AAATTACTTT ATCAACCAGC TGTATTGTTT CCCTCTTGTA AAAGTACCAT CAAGTGGGGA 240  
AAATGTATGT GGCAGTCTCG AG 262

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
GAATTCGGCC TTCATGGCCT AATAACTTAC CCAGTCACGA ATATTTCTTC ATAGCAGCAT      60
CAGAGTGGAC TAATACGATT ATAATTATCA TCACCTTTTG ACTGACCAAT TGATTTACAG      120
TATTGAGTTC AATCTGTTTT TTTAAAAAAT ATCTTCTAAA TATCAGGTGC TGTATTAGAT      180
GTGGGGTACA AAAATGTATT TTCATTTACT CACTAATTTA CTTAAATTTT ATTTATTGAG      240
GTACCTCGAG                                         250
```

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GAATTCGGCC TTCATGGCCT AGGTGCTGGA AGTAAGCTGT GTGAACAAAT GAGACGATTC      60
CCCTTTCTAA TGAGTTTATA TGCAATGTGG TATCTTTACC GATACATGCT CTGTCAGAAA      120
GAAGCAGCCC ACTTCTGTCC AATAGCCAAT CCGGCTTCAG GAGCAGCAGG AGAGGCTTCG      180
GGAACGGGAG AAGAGGCTTC AGCAGCTGGC CGAGCCACAG AGCGACTTGG AGGAGCTGCA      240
CGAGAACAAG AGCGCACTGC AGTTGGAGAG CTCGAG                                         276
```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GAATTCGGCC TTCATGGCCT ACTCATTCCA AAATAAAAAA AAAAATTTCC CATGATCTTA      60
TCTAGCTTCT CTAGCAGTAC TTGTATGATT TCACCTTTCT TTCTTTATTC TTTTCTTCCA      120
TATTTTITTT TTTTGAGACA GGGTCTCACT CTATTGTCCA GGCTAGAGTG CAGTAGTTTG      180
ATCATGACTC ACTCTAACCT GGACCTCCGG GGCCTAAGTA ATCTTCCCAC CTCAGCCTCT      240
CAAGTAGCTG GGACTIONAGG GATGTACCAC CATGCCTGGC TAAG                                         284
```

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

GTTGAATTCT AGACCTGCCT CGAGGACGCC AGGGAAGTGA GTTGAAAATC TGAAAATGCG      60
GCCATGGACT GGTTCCTGGC GTTGGATTAT GCTCATTCTT TTGCTCTGGG GGACCTTGCT      120
GTTTTATATA GGTGGTCACT TGGTACGAGA TAATGACCAT CCTGATCACT CTAGCCGAGA      180
ACTGTCCAAG ATTCTGGCAA AGCTTGAACG CTTAAAACAG CAGAATGAAG ACTTGAGGCG      240
AATGGCCGAA TCTCTCCGGA TACCAGAAGG CCCTATTGAT CAGGGGCCAG CTATAGGAAG      300
AGTGCGCCTT TTAGAAGAGC AGCTTGTTAA GGCCAAAGAA CAGATTGAAA ATTACAAGAA      360
ACAGACCAGA AATGGTCTGG GGAAGGATCT CGAG

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

GCTGTGATGA AAATGCTTTA TGCTTCAACA CTGTTGGAGG ACACAACGTG GTTTGCAAGC      60
CGGGCTATAC AGGGAATGGA ACGACATGCA AAGCATTTTG CAAAGATGGC TGTAGGAATG      120
GAGGAGCCTG TATTGCCGCT AATGTGTGTG CTGCCCACA AGGCTTCACT GGACCCAGCT      180
GTGAAACGGA CATTGATGAA TGCTCTGATG GTTTTGTTC AATGTGACAGT CGTGCTAATT      240
GCATTAACCT GCCTGGATGG TACCACTGTG AGTGCAGAGA TGGCTACCAT GACAATGGGA      300
TGTTTTCACC AAGTGGAGAA TCGTGTGAAG ATATTGATGA GTGTGGGACC ACTCGAG       357

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

GAATTCGGCC TTCATGGCCT ATTTCCGATC TATGTATCTG TACTCATACA GCCTCATCGG      60
GCTAAACAGC CTTCTTTTCA GAACAGTAGA TCACTCAACT GGGTTTTCAG GTGACTGTTT      120
ACCTTTCAAG GCTGGCTTTA TAGGTCTTGC CTCACGTGAT CCAGCAATCC AACTTTTACC      180
CTATCCCAGT CAGGACTGCA CACCTCATAT TGAAAGACAT ACCTTAGAAC CAGACTCCCC      240
AAACCTTACA AATATCCCAC CCTTGACTCC CGTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTAGA	CCTGCCTCGA	GCGCCACACA	GTGACTGCCG	GGTAAAGTTG	TGGAATTACG	60
TCCCTGGACT	CACCCCCTGC	CTTCCTCGCC	GAGTCCTGGC	CATAAAGGGC	CGCGCCACCA	120
CCCTGCCCTG	ACCCTCCCCA	ACTCTCCCTG	TCTCCTCTTT	CATTCTTCCC	CTCTTTCCTT	180
TTCCCTCTCT	TTCCCCACTT	CGATATGAGC	TGCTTCTTAA	CGGTATGAGA	TTATTINACT	240
CCTTCTTCTT	CCTTTCCTTT	CCTGTCCTGC	CTGGCCTAGA	GAGGTGCCCT	GCCTGTCCCT	300
CCTGCACCCA	CCGTCTTTT	CCAAGCATGA	ACAGTGGGAC	AGGCCCCAGG	AGATGGGTGC	360
CAGGGAGCAG	AAGGGGGAGC	CTTCAGGCCT	GGACAAAACG	AAACACCCCC	CCAAAAAAG	420
NAAACCCACG	ACTCGAG					437

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTTCTTCTA	AGTAGATCTT	CCTTCCCCAT	TAAACTAGGT	TTTCTACTGC	AAGATATTTT	60
GTGCATTGCT	GTTTTAAACC	CTTTTAACAG	CGAATCATAG	CAGTCTAAGA	AGTCTTCTGA	120
ACCATCCTGG	ACTCTTGGTG	TGATTTTAAA	TTGTGTCTAC	AAGTTCTCTG	ACATTCTTCC	180
CACCAAGAGG	TAGAGTCTGT	TTCCCTCCC	TTGAACCTA	GGTAGGCCTT	TGTTACTGCC	240
TTGATGAATA	CAATGAGACT	CGAG				264

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTTTTTAC	CCAAAGCTCT	GGAATTGTAC	ATTATTTTTT	TAAAACTCAA	AGAGGGAAAG	60
AGCCTTGTAT	CATATGTGAA	CATTGTATCA	TAGGTAATGT	TGTACAGACC	CTTTTATACA	120
GTGATCTGTC	TTGTTCTGTC	AGCAAAAATC	CTCTATGGAC	ATAGGAGGTG	CTGTGTCCCA	180
TGCCCTCTTG	CCCTGACAGT	GTCCCATGGG	CCCCCTTCTG	CTCCCTGCCC	CCTCCCTGCT	240
ACTGCTGATG	CACTCCCCCC	CCTCGAG				267

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCGGCC	TTCATGGCCT	ATTTTTTATT	TGTTTTGTTT	TGTTTTGTGG	GGATGGGGTT	60
TTGCCGTGTT	GCCCAGGCTG	GTTTCGAATT	TTTGGGCTTA	TGCAATCCAC	CCACCTTGGC	120
CTCCCAAAGT	GCAGGGATTA	CAGGCATGAG	CCATCTTGCT	GGGCCACCTT	TTCTTCTCT	180
TTTAACAAAT	TCAGCAATTT	TTCAGTCCCA	GAAATCTGTA	AATACATTTT	TTGTGGAAAA	240
ATACAATGGG	AATGGCATCA	AAAGATGGTT	TCTATTAGGA	ATGGGAACAG	GTAACAGTTT	300
TCCTTGCCAC	CTCAACAATC	TCGAG				325

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGCTGGCAG	GCGGGCCAAA	GGTAATGAAG	CAAAGAGAGA	GGGAAAAGAC	GTGTGAAAAT	60
TGCAGAGGGG	GTGACCGAGG	GAAACACGTG	AGCGTGATAA	TGACAGAAAA	ACCACGGAAG	120
GAGCAAACCT	GGGCAGGGGG	TGGGAAACCC	GGGCCGTTTC	CAGGGAGCAC	AGGCAGACTC	180
AGAGGTAACA	CTCAAAAGCA	ACAACAGAAG	CAAGGAGGAA	GTGGGAAAAT	ATTTTAAATG	240
TGCTACAACG	AAACAGCTGC	CTGAATTCTA	TATACCTCTT	GAAAATAATC	TGCACATAAA	300
ATGGGAAAGC	TCACCGCAG	CAGACCCAC	TCGAG			335

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCC	TTCATGGCCT	ATGCTTCTTC	CACGCACCAC	CACCACCACC	ACCACCATCA	60
TGGCCATAGC	CACGGTGGCC	TGGGGGTGCT	GCCTGATGGG	CAGTCCAAGC	TCCAGGCCCT	120
GCATGCCCAG	TATTGCCAAG	GACCGGGCCC	TGCCCCGCCA	CCCTACCTCC	CACCCAGCA	180
GCCTCTCTT	CCCCACCTC	CCCAGCAGCC	CCCACCTTG	CCCCACCTGG	GCTCCATTCC	240
ACCGCCTCCC	GCCTCAGCCC	CACCTGTGGG	GCCACATCGC	CACTTCCACG	CCCATGGCCC	300
AGTCCCAGGG	CCCCAACACT	ATACCTTGGG	CGGGCCAGGC	AGGGCACCCA	GACGGGGGGC	360
TGGAGGACAC	CCTCAGTTTG	CTCCACATGG	CCGCCACCCC	CTGCACCAGC	CCACATCCCC	420
ACTGCCCCTG	TACAGTCCTG	CCCCCAGCA	CCCTCCAGCC	CACAAACAGG	GCCCTAAGCA	480
CTTCATCTTC	AGCCACCACC	CATCTCGAG				509

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCC	TTCATGGCCT	AAAGATGGCG	GAGAACAGCG	GTCGCGCCGG	CAAGAGCAGC	60
GGGAGCGCG	CGGGGAAGGG	GGCGGTGTCC	GCAGAGCAGG	TGATTGCTGG	CTTCAACCGC	120
CTTCGGCAGG	AACAGCGAGG	CCTGGCATCC	AAAGCAGCTG	AGTTGGAGAT	GGAGTTGAAT	180
GAGCACAGCC	TAGTGATCGA	TACACTGAAG	GAGGTAGATG	AAACTCGTAA	GTGCTACCGC	240
ATGGTTGGAG	GAGTGCTGGT	GGAGCGAACT	GTCAAAGAGG	TGCTGCCCGC	TTTGAGAAAC	300
AACAAGGAGC	AGATACAGAA	GATCATTGAG	ACACTGACAC	AAGCAACTCG	AG	352

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGCC	AAAGAGGCCT	AGCTAGGTTT	TGAAGCTTCT	GAGTTCTGCA	GCCTCACCTC	60
TGAGAAAACC	TCTTTGCCAC	CAATACCATG	AAGCTCTGCG	TGACTGTCTC	GTCTCTCCTC	120
GTGCTAGTAG	CTGCTTCTG	CTCTCTAGCA	CTCTCAGCAC	CAATGGGCTC	AGTCCCCCCC	180
CCCGTACACG	CCTCGAGGCA	GGTCGAG				207

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCC	TTCATGGCCT	AGGCGGGACT	AACACAGGGT	TGTCATCTTT	TCCTTTTGCC	60
AAGAAAGAAC	ATTAAATGT	ACTACCAGCA	TCTGCCATCA	CTAGCATTTC	ATAAAAAGAG	120
GTTCTGTTAG	CAACAGAGTA	GAAACTGTAG	GAAAGCATCT	CAGAACAAAA	CTAAGTTGAA	180
TAAATTCACC	TAATAAAAAT	GCCTTGGTCT	AGGATTCCTT	TTCTTCATCA	AAAGCTGCAA	240
GAGAAAGCCA	CTGCTTACCT	GATGCCGATT	TACTGGTCAT	TGGGGTGGGC	AGGTTTGGTT	300
CTCGAG						306

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCTCACTT	GTCTCATCCT	GTCGCCCAGG	CTGGAATGCA	GTGGTATGAT	CTCAGCTCAC	60
TGCAACCTCA	GCCTCCTGGG	TTCAAGTGAT	TATCCTGCCT	CAGCCTCCAA	GTANCTGGGA	120
CTATAAGCAC	ACATCACCAC	ACCCAGCCAA	TTTTTTTGAA	TTTTTAATAG	GGTTTCACTA	180
TGTTGGCCAG	GCTGGTTGAA	CTCCTATCCT	CAAGCGATCC	ACCCACCTCG	GCCTCCCGAA	240

GTGCTGGGAT TACCTGAGCC ACCGTGCCCCA GCCCATTTCA CAGTACTTTT TATTTAACCC	300
TATCGTGCTA GGGCACCATG CAATATACAG CTATTTCATT TTCCTTTTGT CTCTGTTTCT	360
TAGGTGGTCT CGAG	374

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAATGGCAG GAATTCGAAA TATTGGCATA TGGTTCTTTT GGATTAGATT ATATAAAATC	60
AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTCTCT GCATGATACT TCTGCTTATT	120
GTCCTTCACA CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC	180
CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT	240
TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGACG	300
CTCGAG	306

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTAGAGATA ACAAACAGG ATACCAAAGT TGAGCTGGAG ACTTACAAGC AAATCGGCA	60
AGGTCTGGAT GAAATGTACA GTGATGTGTG GAAGCAGCTA AAAGAGGAGA AGAAAGTCCG	120
GTTGGAAC TGAAAAAGAAC TGGAGTTACA AATTGGAATG AAAACCGAAA TGGAAATTGC	180
AATGAAGTTA CTGGAAGAGG ACACCCACGA GAAGCAGGAC ACACTAGTTG CCCTCCGCCA	240
GCAGCTGAAA GAAGTCAAAG CGATTAATTT ACAGATGTTT CACAAAGCTC AGAATGCAGA	300
GAGCAGTTTG CAGCAGAAGA ATGAAGCCAT CACGCTCGAG	340

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCGGCC AAAGAGGCCT AGATTTTAAA TTGTTTGAT ACCTGCTGTG TATTCCTTGC	60
ATACCCAGCA CATTGTTGCC CATATTGTTG ACATGTAGTA TGTATTTATT ACAATTATAT	120
GATTAATGAA ATGTATCTTA TTTTTCAT GTATAGCATG TACAGTCACA CTCGAG	176

## (2) INFORMATION FOR SEQ ID NO:24:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

GAATTCGGCC AAAGAGGCCT ATTCTTTGTC TTTTGACAT GTTCTTTGAG TCTTAGTATC      60
TGTAACGTGG CGCTACTCTC TCTATCATGG GGGGGCATGT TTTGACATTA AATTGACTTT      120
TAAGAAAAAC ATGTCATAA CCTGAAGCTC AGCCACACAG TGACTTTTAA GGTTTTATTT      180
AGACTTTACT GTTGTCTCA TGAGAGTAGG TACAGACTGC ATAAGGTTTA GAATCCCAGC      240
ATATGTCTGA AACGACGGGA CTTTCACTGT GATTTCACC AGAGAAATTA TAGCAGAGTG      300
GCTGAGCATG TGCTCTGAGG CCAGGCCCCA GCTCTGCTGC TGACGAGCTG TGTGGTCCTG      360
GGCAGAGTGG TCTCCGAGTT CCAGTCCCTC CTCTGTAAAA TGGGCTTACT CGAG          414

```

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

GAATTCGGCC AAAGAGGCCT AAACATATAC CTAGTCTATA CTCTCTCTTA TCTCTGAACA      60
CTTTTCATCT GGAGCTATTA ATGCCCTCTA GCCTTTTATTA TAATTATCAC ATATAATTAT      120
GCCTTTTCTC CTCAAAATTA TCTGTTGGAG TCATCTTATA GTAGAGTCTT TACAGAACAC      180
AAAGCATTC AATCACTTAT TTCAGACACC AACCTTGTTT TTGATGAACA TATGTTAGTC      240
TTAAGCCATC TAAAGTAATG CTAATGTGGG ATCTTATGGA AGACTACTGG TAATACAGGA      300
AAAAAAGTGG CAAAGAAATC TGACACGTTT GGCAATTATT CCTGAGGCTC TGACCTCTCA      360
ATTGTTGAGT GTTGGAGGTC ACAGTAAACA AACCATATAA AGATCATGTT GAAAGTCAAC      420
ATTATTAATA TACCATACTT GAAGGATATG TGGTTATTGT CTCACGTGTC CATGTGAAGA      480
GACCACCGTC CCTCGAG          497

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

GAATTCGGCC AAAGAGGCCT AGTTTTTGAT GAATTTGTGT TATTACTTAA TAACTAGAGT      60
TTGAATGTTT ATTGGGAAAA CTTAATCATG ATCATCTACT GGTGGCTCGA G          111

```

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCGGCC	AAAGAGGCCT	ATGCAATTCT	GACCAGGAAG	CTCCTCTTTA	ATTGGAAATT	60
CTTAGAAAGG	TATGGAGCAA	AGGAGATCCC	AGCAAACATT	CCGGCATCTA	CTGCTCTTGG	120
GTTTTTCTG	TGTTGGTTTT	TTTTGTTTTG	TTTTGTTTAT	GAGATGGAGT	CTCACTCTGT	180
CGCCCAGGCT	GGAGTGCAGT	GGCGCAATCT	CAGCTCACTG	CAATCTCCAC	CTCCAGAGTT	240
CAAGTGAATA	TCCTGCCTCA	GCCTCTCAAA	CAGCTGGAAT	TACAGGTATA	CACCACCACA	300
CCGAGCTCGA	G					311

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCGGCC	AAAGAGGCCT	AAGTGCAGTG	GTGCGATTAT	AGCTCACTGT	AGCCTCAGAA	60
TCCTGGGCTC	AAGCTGTCCCT	CCCACTTAGC	CTCCCAAAGT	GCTGGGACTA	CAGGCGTGTG	120
CCACGGGGCC	CAGCCATTTT	TTCGAATATT	TTCAATCTGC	AGTTGTTTGA	ATCCACAGAT	180
GCAGAACCCA	TTTCTAATGG	AGGGCTGACT	ATACCTTTCT	GATGACCTAA	ATATTGTGTG	240
CCACTATTGG	GACACTCCTT	TCTTAGTGTC	AAGGTTTGTC	AGAAATTGAG	GGCTGTTTGA	300
TGGGCAAGA	TTTATTTATT	TATTTACTGG	CTTATCTACA	ATTGAGACAG	GGTCTCACTA	360
TGTTTCTCAG	GCTAGTTCTA	ACTCCTGGGC	TGAAGCAGTC	CTCCCATCTC	AGCCTCCAG	420
AGTGCTGGGA	TTACAGGTGT	GACACACCAT	ACCCGGCAGA	GCAAAGAGTT	AAGAGTACAA	480
GACATTTGAT	CATCTTGAGG	AGTATTTACT	TCAGACTGAA	ACACCACATG	AAATTCTAGA	540
GTCCAACAGA	AAGTGTAAATA	ATTTTTTGCT	TTCCCTTCT	TCCGCTACAT	CCTCGAG	597

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCGGCC	AAAGAGGCCT	AATTCTAGAC	ATGCTCAGCT	TTGTGGATAC	GCGGACTTTG	60
TTGCTGCTTG	CAGTAACCTT	ATGCCTAGCA	ACATGCCAAT	CTTTACAAGA	GGAAACTGTA	120
AGAAAGGGCC	CAGCCGGAGA	TAGAGGACCA	CGTGAGAAA	GGGGTCCACC	AGGCCCCCCA	180
GGCAGAGATG	GTGAAGATGG	TCCACAGGC	CCTCCTGGTC	CACCTGGTCC	TCCTGGCCCC	240
CTGGTCTCGG	TGGGAACTTT	GCTGCTCAGT	ATGATGGAAA	AGGAGTTGGA	CTTGGCCCTG	300
GACCAATGGG	CTTAATGGGA	CCTAGAGGCC	CACCTGGTGC	AGCTGGAGCC	CCAGGCCCTC	360
AAGGTTTCCA	AGGACCTGCT	GGTGAGCCTG	GTGAACCTGG	TCAAACCTGG	CCTGCAGGTG	420
GTGCTGGTCC	AGCTGGCCCT	CCTGGCAAGG	CTGGTGAAGA	TGGTCACCCT	GGAAAACCCG	480
GACGACCTGG	TGAGAGAGGC	CTCGAG				506

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GAATTCGGCC AAAGAGGCCT AGTCTGTGGT CATTTTCAAC TCTCATTTAT AGGATTCTAA      60
AAGGGCACTA CATTACTCCA CTCCCTTATC TAAAATAAAT TTAAAATTCA TCGGAATTTG      120
TCCAGTCCTC CATCACTGGA AAATGTACAG ATTCCTTCTC TGGAAATATC TAAAGAAAAG      180
TACAGCTAAT GTTCCCCCAT TTCGTGTTGT TTTGTTGCTG CTTTAACTAT GAACTCATCT      240
GGCCGGGGCGC AGTGACCAAG CCGCCGGGAG CTGGGGAGAG ACGCACCGGG GCGGCGACTG      300
GGCCAGGAGA CCAGAACACT CGAG                                         324

```

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

GAATTCGGCC AAAGAGGCCT AGGAGCAGAT TCCTCATGGT GCTTGTTTAT TATATATATT      60
TAATCCTGCT TGACACTTTA CCCAAGGGAG ATGGTCCCTT TTATCAGTTG AATGTTAGCA      120
GCGTTATTTT AGAGTGTGGT GACTGGTTAG AGAACTCAT GTACTCAACC AGCCACAGTT      180
TCAACAAAAA TTTTATGTG CAAAGGACAG CAACCTTCTT GTATGTTAAA CCACCACTAC      240
TCGAG                                         245

```

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

GAATTCGGCC AAAGAGGCCT AGGTGCTTTG GTTTTGTGCT TTTTAGTCAT CCCCATGAGA      60
ATAATAAACT CCATGAGGGC AGCAACTTGG CTGGCCTGTG TGCCAGTGCT GGGGACATCA      120
CTGAGAAATG AAGGCCCAT TGGCAGGCTA TTTTGTAGCA AGATTCCTGA GGCCCAATCG      180
TTGGGTGATG AGATGGACCC GAGGTATTTC ACTCCAGCTC TCGAG                                         225

```

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

GCCAAGAGG CCTAGAGAGC TCTGGGGGGC AACCTGGAGG TCTGAAAAGA GGAGCCAGAG      60
AAGGTGGTAC CAGGCTTCCT GGTGAGAACC GGCCTGGAGC TCCTTCCCTT CCCCCTGGCC      120
TGAGAGGTTG CTTTAAAGTC TTCCACCCCT TGTTCATCT GCCTGCCAAC CCATCGGAAA      180
GGAATCCACA TCATATTGGA GATGACCCCA TCAACCCAGG GGTCCAGCA CTACCAAGTT      240
GGAATTCAC  GCCCGGGAGT GGGGTAGAGG AAGACGAGAC AGGACGAGGC AGAAAAGCAC      300
ATTTTAAAAA CCAGACAAGA TGGCTAGGCC ATCACCACC AACGGACTTA CCTTACATT      360
TTGTAGGTAA TTCCCCCAA ATCTTGATT TTTTTCCT CAATTATCCT TTAAAAATA      420
AGAAAACACA TTCAAACCC ACTCGAG                                         447

```

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

GCGATTGAAT TCTAGACCAT GCCTGCTCTG GGGCCAGCTC TTCTCCAGGC TCTCTGGGCC      60
GGGTGGGTCC TCACCCTCCA GCCCTTCCA CCAACTGCAT TCACTCCCAA TGGCACGTAT      120
CTGCAGCACC TGGCAAGGGA CCCACCTCA GGCACCTCT ACCTGGGGGC TACCAACTTC      180
CTGTTCCAGC TGAGCCCTGG GCTGCAGCTG GAGGCCACAG TGTCCACCG CCTGTGCTA      240
GACAGCAGGG ACTGCCTGCC ACCTGTGATG CCTGATGAGT GCGCCAGGC CCAGCCTACC      300
AACAAACCGA ATCAGCTGCT CCTGGTGAGC CCAGGGGCC TGGTGGTATG CGGGAGCGTG      360
CACCAGGGGG TCTGTGAACA GCGGCGCTG GGCAGCTCG AG                                         402

```

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

GAATTCGGCC AAAGAGGCCT AGTGGAAGAT TTGGGTACTG TCTTAAATA ATCAATCAAT      60
CGACTCTTAT TTCAAGGAGA AAGTTCTATG TTATATGTTG AAGGTGAACA GATCATATTT      120
AGAGGATATA ACAATTAGAA ATCTAGAAAA TAATTATCAC TTTTATAAAA TTTTGTAGTCA      180
ACTGTACAAA TAATTACATA AAACATCAAT TAATTATGCT TAAAAATCAC TAATGTTTAT      240
AATATATAAT CACTATTTGT AATCAAAAGT TTAATTTTAT GCCAAAAAT AAAAAATGCT      300
TACTCGA                                         307

```

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCC	AAAGAGGCCT	ACTTCCATAA	CCGTGCTTTT	GACGTTAAAA	ATTTTAAATT	60
CAGCCTTTTG	GAGAACACTA	AGTATCTTAG	TGTGTTTTTA	CTTACTATAA	TAATATTATT	120
GACCTAGTGT	AATATTACTG	CCATATGGAC	CTCAAGGGTA	CTTTTCTGAT	AAATTTCGT	180
TATGGTTTCA	TAATTAAACA	AAAGGATAAT	ATACAGAGTT	GTGGAGTTTT	TTTGGTTTTG	240
TTTGTTTTTG	AGATAGCCTG	GGCAACGAGT	GAAACTCTGT	CACACACACA	CACACACACA	300
CACAGACACA	CACCAAATCT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGGCT	TCATGGCCTA	CAAGAAGATG	AAGAAGATTG	TGGATGCCGT	GATCAAGTAC	60
AAGGACAGCA	GTGGACGTCA	GCTCAGCGAG	GTCTTCATCC	AGCTGCCCTC	GCGAAAGGAG	120
CTGCCCGAGT	ACTACGAGCT	CATCCGCAAG	CCCGTGGACT	TCAAGAAGAT	AAAGGAGCGC	180
ATTCGCAACC	ACAAGTACCG	CAGCCTCAAC	GACCTAGAGA	AGGACGTCAT	GCTCCTGTGC	240
CAGAACGCAC	AGACCTTCAA	CCTGGAGGGC	TCCCTGATCT	ATGAAGACTC	CATCGTCTTG	300
CAGTCGGTCT	TCACCAGCGT	GCGGCAGAAA	ATCGAGAAGG	AGGATGACAG	TGAAGGCGAG	360
GAGAGTGAGG	AGGAGGAAGA	GGGCGAGGAG	GAAGGCTCCG	AATCCGAATC	TCGGTCCAGT	420
CTCGAG						426

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCGGCC	TTTATGGCCA	ACACATAATC	CACGCTCATC	TTGCAAAGCG	CTATTTTCAGG	60
CACATCATTG	GAATACAGGA	AGTAGCCCTG	CACCTGCCAG	TGAGCTCGCC	ATTCAGTGAT	120
TGGAAGAGTG	ACCTGGCATC	TTGGAATCA	TTGTGTGTCT	TCAGGAGAAT	GTGCAGTGTC	180
TTGTAACAAC	TAATTATAAT	GCAAATTAGG	GCTACATTGT	AATCTGCTTT	GTTAATGAAA	240
ATGATAAAAC	AGAATATTGA	CAAGCTAGGA	CACCTGTGGT	ATCTTTAATT	GTATCTCCTT	300
CAGAAGTTTG	CTTCTTATGG	TATAATAAAG	TATGGAAGAA	TATTGAGTAT	ATGTTTACTC	360
TGGGCCTGGG	AGAACTTAAC	TTTCTAGAGC	AGTTTGTGA	CTTGTGTGCA	ATGGGGAGAG	420
GTACCATGAT	GAACTCACA	GGGAGCCACT	GTTCACTGAC	ACTTGAAGG	CCCTGCCTCG	480
AG						482

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GTGTTTGCCC ACACCCTCCT TGAATTAAAC TGCCACAATC TATCCGCAGA TGTGTTTGT      60
TCGTGTTTCTT GTTTTTCAC TACGTTTGCG TTGCTTCCTC TGAAGCCAGA GGGTGAAAGG     120
CCCTAGCAAA GTTAGTTATC AGTCAACTGA TGATAACTGT GATCCTTAAA GATGAATTCC     180
CAGCCTGAGG TGACACACAG AGGTTTCAGCA GACGTCTCAG GATCTGTCAC ATGTCATGTT     240
GCTTGGTGTG AAGATGGAAG AACAAAGTCC ACATCAGTTT CTGCTCCTTC AAACAGTGTG     300
TCGATATGAA ACATTGAGAT TTGGCAGAAA CATGTGCCTA GTTTGCAGCA CCAAATACTC     360
GAG

```

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

GAATTCGGCC TTCATGGCCT AAAGGGATAT TCACTCAAAT CCCTAAGTAT TTCAGAAACA      60
GCCTGAGAGC AAGTCCTTGG CTTCGCTTTC TAGTTTAAAG AGGCTTTTAA CTGTTTAGTC     120
TGAGATTCCC CTAAAAGTTC CAGGAAAGCA AACTCAAAAA GAGCCTAGGT GGTCAATCAT     180
TATTTTGGCT GCGTTTATAT AAATAATCAG GCCAAGTTAA TGAGACTAAA CTTATTTTGC     240
AAGCAAATCA GTCTTTGCTT ATTTTGGTA GGAATGGGGG TAAATGGAGA GAGAGAAATT     300
ATGTTTCAGA AGAAACTAT AGCACACCAA CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GAATTCGGCC TTCATGGCCT AGTGGGAAAC ATTATTTCAA GACATTAGGG ATAAGAATGC      60
CAGTTGCTAC TGAGTTGGTT ATTGTTTCAA GGATTATCA ATACATAGAG CAAATAATTA     120
TGTTTTGCTT TGTCTTATTT TTATTTCTTT ACTTTAGAAA CAGTACAGCT ACTTACAAAT     180
CAAGTTTAGA ACTCTCAGGT TATCTTAAAT CTGAAGCTTC TACCTTCCTA AGAACAAAC     240
ACCGGCTCGA G

```

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

GTTC AACAG TTCAA TACT TTTCA ACCT CTATTTCTTA CTTCCTGCCT GCTCTCAGTT      60
TGTTCCCGAA ATGAGACTTG GTGCACTCTA TACCTACTGG GTTCCCCTGG GCTTCGTGCT      120
GGCCGTCACGT GTCATCCGTG AGGCGGTGGA GGAGATCCGA TGCTACGTGC GGGACAAGGA      180
AGTCAACTCC CAGGTCTACA GCCGGCTCAC AGCACGAGGC ACAGTGAAGG TGAAGAGTTC      240
TAACATCCAA GTTGGAGCCC TCAGAG                                     265

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

GAATTCGGCC TTCATGGCCT AAGATGATTG TGCTATTATT GTTTCGCTTG CTCTGGATGG      60
TGGAAGGAGT CTTTCCCAG CTTCACCTACA CGGTACAGGA GGAGCAGGAA CATGGCACTT      120
TCGTGGGGAA TATCGCTGAA GATCTGGGTC TGGACATTAC AAAACTTTTCG GCTCGCGGGT      180
TTCAGACGGT GCCCAACTCA AGGACCCCTT ACTTAGACCT CAACCTGGAG ACAGGGGTGC      240
TGTACGTGAA CGAGAAAATA GACCGCGAAC AAATCTGCAA ACAGAGCCCC TCCTGTGTCC      300
TGCACCTGGA GGTCTTTCTG GAGAACCCCT TGGAGCTGTT CCAGGTGGAG ATCGAGGTGC      360
TGGACATTAA TGACAACCCC CCTCTTTTCC CGGAGCCAGA CCTGACGGTG GAAATCTCTG      420
AGGGCGCCAC ACTCGAG                                     437

```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

GAATTCGGCC TTCATGGCCT AGTACCTTAA AAACCTTGGA AATAATAATA ATAATAATAA      60
ACAAAAAATA ATCCCAAACC CCGTAAGTTT AACTTTCTAT GCTTTGGCTG TTTTGGTTT      120
ATTTTTTGT TTTTAGAAGG GGTCTCGCTC TGTCGCCAG AATGGAGTGC AGTGGCTTAA      180
TCAGGGCTCA TTGCAGCCTC GACCTCCTTG GTTCGGGCGA TCCTCCTCCC TCCACACTCG      240
AG                                     265

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATTAAATTA	AAATTAAATC	TTTGTTACAA	ACTATGAAAA	TGAATATAAG	TAAATTTTCAT	60
ATCATTTTCTT	TTCTAGATTT	ATTATCTAGG	ATAGATTGG	ATGAACTAAT	GAAAAAAGAT	120
GAACCGCCTC	TTGATTTTCC	TGATACCTG	GAAGGATTG	AATATGCTTT	TAATGAAAAG	180
GGACAGTTAA	GACACATAAA	AACTGGGGAA	CCATTTGTTT	TTAACTACCG	GGAAGATTTA	240
CACAGATGGA	ACCAGAAGCT	CGAG				264

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCGGCC	TTCATGGCCT	AACCTGGAGA	AACTATTAA	GTTGGATGAA	GCAAGTGCCC	60
AGCTCCTTGC	TTATAAGGAA	AAAGGCCATT	CTCAGAGTTC	ACAATTTTCC	TCTGATCAAG	120
AAATAGCTCA	TCTGCTGCCT	GAAAATGTGA	GTGCGCTCCC	AGCTACGGTG	GCAGTTGCTT	180
CTCCACATAC	CACCTCGGCT	ACTCCAAAGC	CCGCCACCCT	TCTACCCACC	AATGCTTCAG	240
TGACACCTTC	TGGGACTTCC	CAGCCACAGC	TGGCCACCAC	AGCTCCACCT	GTAACCACTG	300
TCACCTTCTA	GCCTCCACG	ACCCTCATTT	CTACAGTTT	TACACGGGCT	GCGGCTACAC	360
TCCAAGCAAT	GGCTACAACA	GCAGTTCTGA	CTACCACCTT	TCAGGCACCA	TAGTGACTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAATTCGGCC	TTCATGGCCT	ACCGAAGGGC	ATCCCATCGG	TTGGGTAGGT	CATGGTTAAA	60
AAATCATCTC	CTTTGGTTGC	ATATTAAATT	ATTTTCCACT	ATTTTTCCT	CACACAAAAT	120
GATTTTGCCC	GGTACCCTTT	TTGGGGGTGC	ACAGTCCATG	AGATGAATAT	TGAATGGGGA	180
GACCTGGGTT	CTAGTCTCGC	ATTTACCAGT	CAGGTTACAA	TGCGACCTTG	AGCAAGTCAC	240
TTCACTCCC	AGCGCCTCAG	TTTCCTCATT	GTAAGATAGG	AAAAGCCTTG	TCATTTTAA	300
AATTTTATTT	TTTGCATATA	CCTCATGGCG	AACTCGAG			338

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCGGCC	TTCATGGCCT	ACTATGCTCT	GCACGTGGGT	CATTTCTTAC	TGGTTTCTAA	60
AAGCCTTTCA	TTTTCTGCCT	GTACACAATA	GCCCCCTTCC	TCCATTGTTT	TTAGGATCCT	120
TTTTCCTCTT	ACCAGCTGTT	AACCTGGAAG	TATTTCTTCT	TCATCCCGAA	TCTCCCATGT	180
CCTCCCCACT	TCTATTGTTT	TCCATCCAAT	GTGGATTCAT	GATCATTTTA	TGGATTTTAA	240
ACTACTCTGG	GGCTACCCTC	GAG				263

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCGGCC	TTCATGGCCT	AGAAACACAT	GTGATCTGTA	CTCATGAGAA	CCTGTAGTTA	60
ACTATACGAG	CCTTGCTGTG	CATTTTGTTC	TTATCTGAGC	CTGTCTTTCA	ATGTCCTATC	120
CCTTGAGAGA	ACTGAGGGCT	GAGAACCAAG	CTTTCGGAAG	CGGTCTGAGT	GTCAGCGGTG	180
GTAGTGGTCT	CTGAGAAAAA	GAATGGAGAC	AGGATAGGAC	TTGAGAAGA	GTGAGTCATT	240
GTTACCCAGA	AACCCTGGAG	AACACTGGAC	TCGAG			275

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGCGTTCTC	ACGCCGCAA	CAATTCCTGA	GTAGGGCCTT	GCTTGAGTTC	TTCGGAAAGT	60
CTCATCCACC	CCCACATCGC	CTCITTAGGA	AGTCACCTAA	TGTTGGGCTT	CATTATTCCT	120
ACATCCCTTT	CCTTACTACT	TGCTGCACT	TCTTGAGAAA	AAGACTGCAG	AAAGGAGAGG	180
TGGGGCTTTC	AGTAGAAACA	AGCAAACCGC	AGGTCCCTGT	GGGGGGACTC	TCCAGGAAGA	240
AGGGTAATTT	CCTGCCTCCT	TAAATTGGCT	GCTACTGTCA	GTTATTTTGC	TCCCAACCCC	300
AGAGCTTCAC	TTGCTCCTTC	ACTTCCCACT	TCCGCAAGAA	CCGTGGGCGA	CAGTTATGGA	360
GAAGCGTCTG	CAGGAGGCTC	AGCTGTACAA	GGAGGAAGGG	AACCAGCGCT	ACCGGAAGG	420
GAAGTACCGA	GATGCTGTGA	GATGGTACCA	TCGAGCTCTG	CTTCAGCTGC	GGGGTCTGGA	480
TCCGAGTCTG	CCCTCTCCGT	TACCTAATCT	CGGACCTCAG	GGCCCGGCCC	TCACGCCTGA	540
ACGACCTGCC	TCGAG					555

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGAAGATGG	ACTGCTCTGG	GGCCCATGTG	CAAGTGACCT	GTGCCAAGCT	CATCTCCAGG	60
ACAGGCCACC	TGATGAAGCT	TCTCAGTGGG	CAGCAGGAAG	TAAAGGCATC	CAAGATAGAA	120
TGGGATACGG	ACCAATGGAA	GATTGAGAAC	TACATTAATG	AGAGCACAGA	AGCCCGAGAT	180
GAACAGAAAG	AGAAGTCGCT	TGAGCTCAAA	AAAGAAGTTC	CAGGATATGG	CTATACTGAC	240
AAACTCATCT	TGGCATTAAAT	TGTTACTGGA	ATACTAACGA	TTTTGATTAT	ACTTTTCTGC	300
CTCATTGTGA	TATGTTGTCA	CCGAAGGTCA	TTACAAGAAG	ATGAAGAAGG	ATCACTCGAG	360

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATTCGGCC	TTCATGGCCT	AGCTCCTGCG	TAAAGGAGCA	TGAGAGCGTG	GGAGTTTTCG	60
AGTGGCCGTG	GGGTTCTTCG	TCGCGTCTCG	GTGCGGCGTC	GCTTTCTGCA	GCTCCTGTCA	120
GGGAGCGCGA	GGCCTGTAT	TAACCGCGGA	GCGCTTTGTC	ACGAANTCCC	TGTGGCGTCT	180
TGAAGAAGGC	ATTCCCACC	CGCCAAATGG	CGTCCATGCC	CCCGACGCCC	GAGGCCCAGG	240
AGAGTCGAGG	TACCTTTTTC	GTCCAAGTTT	ATNGCTGCTT	TCGGTCTCTG	CCTGACCCCN	300
TCCTTTGGAG	GAGAGTTGGG	CATGCCTGTT	GTGGTAGGAG	TGCTCNTGAG	CCCCAAATAG	360
CCCTTTGACC	AAGTGTTCCT	CGTTCCAAGA	CCACACACAT	AATGGTTTAC	CAACTTCNTT	420
CTTTCAGAAC	TACCAACTGG	GAGCAGGGAC	CTGTGGAGGA	ATCTCTGAGA	GAGTTTCTCA	480
ATGTCTTATC	TGTTTGTTTT	GTTTGTGTTG	GAGATAGGGT	CTGGCCTTGT	CGCTGGAGTG	540
TTGCTTGTCT	GGCTGGAGTG	CAGTGCTGAT	ATCATAGCTC	CGTCTGGAAC	TCAGGGAATC	600
CTTACGCCTC	AGCCTCTCGA	G				621

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAATTCGGCC	TTCATGGCCT	ACAATTTGGA	GCAAGGCTTA	GCAGAAGACG	GCGGCATGAG	60
CAGCGTGACT	CAGGAGGGCA	GACAAGCCTC	TATCCGGCTG	TGGAGGTCAC	GTCTGGGCCG	120
GGTGATGTAC	TCCATGGCAA	ACTGTCGTCT	CCTGATGAAG	GATTATGTGC	TGGCCGTGGA	180
GGCGTATCAT	TCGGTTATCA	AGTATTACCC	AGAGCAAGAG	CCCCAGCTGC	TCAGCGGCAT	240
CGGCCGGATT	TCCCTGCAGA	TTGGAGACAT	AAAAACAGCT	GAAAAGTATT	TTCAAGACGT	300
TGAGAAAGTA	ACACAGAAAT	TAGACGGACC	TCTCGAG			337

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCGGCC AAAGAGGCCT ACATTACTGG GTTAGAAAAC AAAGAGGGAG TGCCCTGCAC	60
ATTTCTTTT GTGCTTTTAA ATGTTTCTTA AGTTGGAACA GGTTTCCTCG GGCCTGTTTT	120
GACTGATTGC TGGAGTGCAT TTGATAGTTA AAAATTACTA ATTGGTTTTA TTTCCCTTCA	180
CACTCTGCCT CCCCTATTTC CCCCAATTGA CCCTAAACCT CGAG	224

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATTTAATGC ATGCTAGCAA CAGCCTTAAC TTTGGATTCA GTTATTTGAA ACACTTTTCC	60
GGCATCTTTC CCTTTCTAAT GTTGTGGGGT GGAAACCGGA TGGCAAATCA CTGTGAGCCG	120
GATACCTCAG CACAGTCCAC CTTGTGTGTG ACTTCACAAA TGGGGGACTT CACAAATGGG	180
GTAAGTGAAT GTTATTACTT TCAAATTTTG ACATGGAGCA TTATGATCAA GGAAATGGAG	240
CAACTCGAG	249

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCTGCGCCGC ACCCTGAGAG ATGGTTGGTG CCATGTGGAA GGTGATTGTT TCGCTGGTCC	60
TGTTGATGCC TGGCCCCTGT GATGGGCTGT TTCACTCCCT ATACAGAAGT GTTTCCATGC	120
CACCTAAGGG AGACTCAGGA CAGCCATTAT TTCTCACCCC TTACATTGAA GCTGGGAAGA	180
TCCAAAAGG AAGAGAATTG AGTTTGGTCG GTCCTTTCCC AGGACTGAAC ATGAAGAGTT	240
ATGCCGGCTA CCTCGAG	257

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAATTCTAGA	CTTTGTCTCC	AGAGCATTGC	CTTTATAAGC	AGATTGGCAC	CAACAGTTCC	60
ATAGTTTAAC	ATCTAGTTAA	GCTACAAATA	TAGTATAAGC	ATTATTAGCA	GCTGGTACTT	120
CTGCTAGGGG	TGTAAATTC	CAGGTGTTAC	ACTGACCTCA	ATCCAATTTA	CATAATTTAC	180
ATAAATGCAT	CTCGGTGGAA	AAATAATCAT	TTTCTTGGA	TATCTCGAG		229

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCGGCC	TTCATGGCCT	ACACTGCTAT	GTATGTTTTT	TCCTTAATGA	TGAAGAGTGT	60
AGATGATGCT	AATAATAGTA	GCTGATGTAC	TGACTTTTAG	CTGTGTGCAA	AGCCATGTTT	120
AAAATACTTT	ACAAGTGTTA	ACTTGTGTTA	TCTTCACAAC	AACCCTAAGA	AGTGGATATT	180
ATTAAAGTAG	ATTTTGAAG	ACTGATCTAT	TTAATTATTA	ATAGATCTGT	CTCATTCTTT	240
TTTTCCCCCA	ACTCGAG					257

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAATTCGGCC	TTCATGGCCT	ACGCGTCTGC	TTGGGAGACC	GTAAGGATAT	TGATGACCAT	60
GAGATCCCTG	CTCAGAACCC	CCTTCCTGTG	TGGCCTGCTC	TGGGCCTTTT	GTGCCCCCAGG	120
CGCCAGGGCC	TTTGTGCCC	CAGGCGCCAG	GGCTGAGGAG	CCTGCAGCCA	GCTTCTCCCA	180
ACCCGGCAGC	ATGGGCCTGG	ATAAGAACAC	AGTATCACTC	GAG		223

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCTAGA	CCTGCATGTC	CCAGTGTGAA	ATTTCAGCAC	GGCATTCTTCT	GCATCCTTTC	60
ATGGCCATCC	AAAGGATTCC	GCTGCAGAAA	TTATTGATGT	GCTATTTTGT	CTGTCTTTGTG	120
ATGCAGGCTG	CTTTGGGCCC	CTGGTCACT	CTTCCAAGGC	TGCAACTCGA	G	171

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

GAATTCGGCC TTCATGGCCT AAAAAGCAAA AGAAAAGTAA AAGGAAGAAA CAAGAACAAG      60
AAAAAAGATT ATATTGATT TAAAATCATG CAAAAACTGC AACTCTGTGT TTATATTAC      120
CTGTTTATGC TGATTGTTGC TGGTCCAGTG GATCTAAATG AGAACAGTGA GCAAAAAGAA      180
AATGTGGAAA AAGAGGGGCT GTGTAATGCA TGTACTTGA GACAAAACAC TAAATCTTCA      240
AGAATAGAAG CCATTAAGAT ACAAATCCTC AGTAAACTTC GTCTGGAAAC AGCTCCTAAC      300
ATCAGCAAAG ATGTTATAAG ACAACTTTTA CTCGAG      336

```

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

GAATTCGGCC AAAGAGGCCT AGAAGAGCAA GCGCCATGTT GAAGCCATCA TTACCATTCA      60
CATCCCTCTT ATTCTGCAG CTGCCCCCTGC TGGGAGTGGG GCTGAACACG ACAATTCTGA      120
CGCCCAATGG GAATGAAGAC ACCACAGCTG ATTTCTTCCT GACCACTATG CCCACTGACT      180
CCCTCAGTGT TTCCACTCTG CAGCTCTCG AG      212

```

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

GAATTCGGCC TTCATGGTCT ATGCTACTCA GTTGGATCTA GCAGAAACAA AAGCTGAGTC      60
TGAGCAGTTG GCGCGAGGCC TTCTGGAAGA ACAGTATTTT GAATTGACGC AAGAAAGCAA      120
GAAAGCTGCT TCAAGAAATA GACAAGAGAT TACAGATAAA GATCAGACTG TTAGTCGGCT      180
TGAAGAAGCA AACAGCATGC TAACCAAAGA TATTGAAATA TTAAGAAGAG AGAATGAAGA      240
GCTAACAGAG AAAATGAAGA AGGCAGAGGA AGAATATAAA CTGGAGAAGG AGGAGGAGAT      300
CAGTAATCTT AAGGCTGCCT TTGAAAAGAA TATCAACACT AAACCTCGAG      349

```

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

GCGGGCTAGT CATGGCGTCC CCGTCTCGGA GACTGCAGAC TAAACCAGTC ATTACTTGTT      60
TCAAGAGCGT TCTGCTAATC TACACTTTTA TTCTGGATC ACTGGCGTTA TCCTTCTTGC      120
AGTTGGCATT TGGGGCAAGG TGAGCCTGGA GAATTACTTT TCTCTTTTAA ATGAGAAGGC      180
CACCAATGTC CCCTTCGTGC TCATTGCTAC TGGTACCGTC ATTATTCTTT TGGGCACCTT      240
TGGTTGTTTT GCTACCTGCC GAGCTTCTGC ATGGATGCTA AACTGTATG CAATGTTTCT      300
GACTCTCGTT TTTTGGTCG AACTGGTCGC TGCCATCGTA GGATTTGTTT TCAGACATGA      360
GATTAAGAAC AGCTTTAAGA ATAATCTCGA G              391

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

GAATTCGGCC TTCATGGCCT AGGGAGTCTG AAGCAATTTT TGAAGAAGAC CAAAAGAAGC      60
CACAAGACGA TGAATGAAAA GGCAATGGAAG CGTTGGTGCA CACAAATCCT CTCTGCCCTA      120
AGCTACCTGC ACTCCTGTGA CCCCCCATC ATCCATGGGA ACCTGACCTG TGACACCATC      180
TTCATCCAGC ACAACGGACT CATCAAGATT GGCTCTGTGG CTCCTGACAC TATCAACAAT      240
CATGTGAAGA CTTGTCGAGA AGAGCAGAAG AATCTACACT TCTTTGCACC AGAGTATGGA      300
GAAGTCACTA ATGTGACAAC AGCAGTGGAC ATCTACTCCT TTGGCATGTG TGCATGGAG      360
ATGGCAGTGC TGGAGATTCA GGGCAATGGA GAGTCCTCAT ATGTGCCACA GGAAGCCATC      420
AGCAGTGCCA TCCAGCTTCT AGAAGACCCA TTACAGAGGG AGTTCATTCA AAAGTGCCCTG      480
C              481

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

GAATTCGGCC AAAGAGGCCT ACGATTGAAT TCTAGATCTG CCGTCTTGG CCTCGCAAAG      60
TGCTGGGATT ACAGGCGTGA ACCACTGTGC CTGGCATATT TGTCTATTAA TTGCTTTTC      120
TTTAGATGTA TTCTAGAGGG GGGAAAATCA GTAGAAGAAC AGTTATGTAA TTCTAACAAAG      180
TTCTCCATGT GTCTTGCCAT CTNGCTTTT CTATCCTAT CAGTACTGGA TGAGAATGTT      240
TATTTCACTG AACTTTGCCA AAGAGTTTCA ACATTTTTTT GTTTAATCAT AGGAGAAAAA      300
GGTTTATCTT ATTTTAAAAA ATTTTATTT AATTCTTTCA TTACAAATGA AGTCCCAGAA      360
GTTGTATTTG TTTCTTTAGG CTGTTCTTAA TTGTTTATTG GAACAGGCAG GGTTTGAAGG      420
AGTGGGGATA CTGGGAAAGC CAGGGTGATG AGAAAATAGG AAAGGGGTCT TGTCATTGGG      480
AGGCCACTAT ACCAGTGGCC CTTGTACCAG GACTAATATG GTACTTTGAA GCTTTAAATT      540
CATTTCTTTA TTCAATAATT TTAGCATCC CAGGATACTC GAG              583

```

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

GAATTCGGCC AAAGAGGCCT AGCTATCCGC TTTGCTATTT TAGTGGCATT ATCAAAATCA      60
CTGGAAGCAC CTGTNGTAAT ATGGTCGGTT CCAAATATAA GCTCCTCTGC CACTCTTCCT      120
CCCATACTAA CATCCATTG  TGCAAGCAGC TGGGCTCTAG TTTCATTCCA TCTGTCATTC      180
TCAGGTAACA GGGACACATG TCCAAGTGT  GGCCCCCGTG GCATGATTGT AGCTTTGTTG      240
ATAGGCATTG CATCTTTTGT GTAATATGCA ATAATGGCAT GACCAGATTC ATGATATGCT      300
GTGATGGTTT TGTTTTGT  ATCAATTCC  ACACTTCTTC TTTCAGGCC  CATTAGAATT      360
TTGTCTTTGG AAAACTCCAG CTCCTTCATG GTAACCATTT CTTTCCATC AACAGCTGCT      420
TTTAATGCAG CCTGGTTCAC AAGATTCTCC AACTCTGCTC CGGAAAAGCC AACAGTACCT      480
CGAG                                         484

```

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

GAATTCGGCC AAAGAGCCTA ATTGAATTCT AGACCGGCCT CATCGTTCTT TGCCTTCCTG      60
GTCACCATCT GCTACGCTGG AAATACATAT TTCAGTTTTA TAGCATGGAG ATCCAGGACC      120
ATACAGTGAT TTACCATTTT GATAATTAAA AGGAAAAAAA AAGGAAGACT CTCACTGTAA      180
AAACAGCTGT AGGTATAATG TATATTCCCA GAGAATTGTA TTAACTAAT TAATGTTTTT      240
TATATTCTTA AATTGCTCA  CAAATTGTGG TTTGTTACAA TTAACTGGA TACTTATTG      300
CAAAGTGTG  TAGCTTATAA TGAACCTCTA AGTATCTTAT TAATGTATTA ATGTCTTCAT      360
AGATCATATT TTCTTAGACA ATGTTTAAAT AGATAAATTG CTAATATTGA GAATGTGTCA      420
AGTTTGTAAG CCTAACTTTT AAGATGCCAG AACTCGAG                                         458

```

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTAGGT GGTGATTGAC CTAAGAAAAA      60
AGTGTCTTAA ATATCTGGAT TCTATGGGAC AAAAGGGCCA CAGGATCTGT GAGATTCTCC      120
TTCAGTATTT ACAGGATGAA AGTAAGAACC GCTCGAG                                         157

```

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

GAATTCGGCC AAAGAGGCCT AGTGGACTGC TACTTCCCTT TAGCACTATA TACAAACATA      60
ACTGCTACTT CCCTTTAGCC CAGGATCAAA ATAATGATTC AGTTAAAAGT TGCTTGCCTA      120
ACAAAATTTC AAAATATGGA CTTCTGTGAA TTGCTAAAAC ACATCCTTTT AACTAGGCAT      180
CTTTAAGTCT ATAGTATCTT TAAAGTTAAT TTCAAAATTT AGCAGAGCCT GGAACACAAA      240
TTATTCAGGA AATAATTCCT GAACCTACCT CTATCTTCAT AAAACGTATT GGGGCAAGAA      300
CTATTCTATT GAATTCTAGA CCTGACTCGA G                                     331

```

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

GAATTCGGCC AAAGAGGCCT ACCATCTGTC ACTAATATCA AAGGAGGGCC AAGGACACAG      60
CCCTGGGGGA ACTTACCAGG TCAACCCACA ATGGGTGAAT TTATAGTTTG TTAGTTAGTG      120
GTCAGTTACC AACTTCTCTG TCTGTCTAAT GCTTTGACTA AAATGTCCAG ATTATTTACC      180
TAGTTAACAA AATTAAAGAA GATTCTAAGA CCAGTTTAGC ATCATTITCT CTGAAGTCCA      240
TAATGAATGT CTGTTAAACT CTCGTCACTC TTATTTAGGT GCTTTTGGGT CATTTGTGTG      300
AGGTTTATTC TCCCAAATCA ATGTCACATA TACGTCTGTA ACTTGTGTTA TCAGCTTCCT      360
TCCTAGGGCT TTAACCTCTT TTCAGTCTTA TAGCATTCCCT TCCATTTTCC TTTCAATTCA      420
CTCCAATAAA AGCTCGACAA ACTCCTGGGA GCCCCTTGGT GCTCGAG                                     467

```

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

GAATTCGGCC AAAGAGGCCT ACGATTGAAG TCTAGATGCA CACATTCAGC TTCTGTCTCA      60
GTCCTGAGAG TGGTTGTGTT TTATTGGCTG ATGAGTTATT TCCACATATC ACATGTATAA      120
GGTATTTGAA TGAAGGTGCT TTGTAGTCAT GACACACTAC TCTTTTACTA ATTATTAATA      180
TCTTAAGATT ACAATTTGAG AGGTAGAGAT GGTATTGTTT TTAATGGGTG TGGGGGGTGG      240
TGATGATAGG TATTTTACC CTGGTAAGTG ACCTACTAGG TTTTATTAAG TGTTGCAACT      300
TGTCCAGTGT GTGGATGGGA TCTCGAG                                     327

```



## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
GAATTCGGCC AAAGAGGCCT AGTGCTGGA TGTATTTGAG TTCACAGTAT TTGTTTTATA    60
GCAGTTTTCG AAGCACATAC TGTGCCACGG ATTTTCCAC ATTATTTTGA GACAAGGGAA    120
CACAGCCATC AAAACTGATA CCATGGCCGG GCGTGGTGGT GGGTGCCTGT AGTCCCAGCT    180
ACTTGGGAAC TCGGACATT CTCGAG                                         206
```

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 184 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
GAATTCGGCC AAAGAGGCCT CCACCATGCC CGGCCTCAAC GATATTGATT CTTTGGGCTG    60
TAGTCAGTAT TGGATTATGA TCAATATTAT CACCATTAT TTTGTTGCTC CAGTCTTCC    120
AGCTGTGGCC AATCCTTCAG TTGGATTCTT GTGCCCCATC AACATTCTCC ATCCTTCTCT    180
CGAG                                         184
```

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
GAATTCGGCC AAAGAGGCCG ACTTTATTAT ACCATACATA CTATAGGTAC CTGGGCACAA    60
GATAGGTCAG GGGGTACTGT ACCCTATTT ACATGCTTAA TCACATCATA AGGTTGCAGG    120
TGGTACTTGA AATCATCACT AATGAGACAG CAAATATGTT AGACTTGCTG GCCCAGCAAG    180
CCACAGAAAT AAGGATCACC ATCTATTAGA ATAGACTGGC TTCAACTCG AG          232
```

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GAATTCGGCC	AAAGAGCCTA	CTAAAATTCC	TTGTTTGTG	TTTTTAATAT	TCCATCGTTG	60
ATAGTTAATA	TTCTTTTNGA	GGTTTTGTTT	TAGACAAAGT	AATGTTTTTC	TGAAATGATT	120
CTAAGACAAT	TGGTCAGAAA	TAGTCTCTGC	TTGTTTGGTT	TATGTTTGGT	CAGTTGTGCT	180
TTGATTATAG	ATGGTTCCTC	ATCTGAGATT	AAAGTGGGAC	AGAACTTCAA	AAGTAAAAGG	240
GTAAATGTTT	GCTGTGATGC	TTATGTGGCA	CATGTGCTAG	TCCTTGATAG	TGGCGAGAAA	300
GATCTTAATT	GCTCAAAGGA	AGTACTCGAG				330

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAATTCGGCC	AAAGAGGCCT	ACAGTGCATT	ATGTTATTTT	GTTATCTCTG	CAGTAACTTT	60
CTATCATGTT	ATTTATTTTC	TTTGTCCTAT	TTAAAGCTTC	TGAGATTATG	GATTTTGTG	120
TCCTTCCCTG	AAGTTAAGTG	TTATCATTCC	TATATAGTAC	TAAGCTGTCT	ACAGAATAGT	180
GGGAGTCTGC	CCTCTTGAGT	TGGGAAGATC	CTAGTTTGAA	TCTTGGCTGT	GCGACTTTAA	240
AGTTCATTAA	CTTCTCTTAG	CCTCAGTCAC	CTGAACTCTG	CAGTGGGGAT	CCTTATGCCT	300
CAGAGTGTCA	TTGGGAGGAC	TCACGAAAAT	ACGCTTGATC	TTTGAGTTCA	GTACCTAGCC	360
TGTATGAGCC	AGCATTAAAG	GGGACAGTCA	TCACGCAGCG	CTTTGCACAC	AGCTCTCAG	420
CCACATCCTT	TGGCTACTGT	TTTGGTAAAT	CTTTACTAGT	AAATGTTTCT	TAAAAGCATT	480
TACATTCATG	GACATGATTC	CCTCGAG				507

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAATTCGGCC	AAAGAGGCCT	AGATTGAATC	TAACTTTT	GCCTCTTCCC	AAGTAGCCTA	60
TTTGAGCTAG	AACAAAACCT	TGTTAGCCAT	TTTGGGAGAG	AATAGGGAAT	CTAGAGAATG	120
AAGATCTGCC	CGACCTGCCT	CGAG				144

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTCGGCC AAAGAGGCCT AACGACGGTA ATCAAGTTTT GCTCCAGAAG CATCAAGAAA	60
CTTAGCTACT GCTTCCAAAT CAGTACCGGT TTCAGTTAAG CCTTGAATAA TACAGTCTTG	120
AAACTGAGTA GGGTCAAACC TCTCTTTTTC ATCTCTTTT CTAGTTTTAA AACGCTGGCC	180
TGATAGCGTT GGCTTTTGCT GCTTTTGATT ATTCATAAAA GACACCCGAA TTTAAGGCGA	240
AGAGGAAAGA GCCAGAAATC CCCGATGTAC CGGCAACTGC GCGCTATCT CCTCGAG	297

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAATTCGGCC AAAGAGGCCT AGACTGCTGG TGGTGAAGTG CTTTCTTGT AGGTTGTGAG	60
GGCTGAAAAA GCCAATCTTA ATAGACATGA GGCTCATGTT TGCACAGTGT GCTCTCGAG	119

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAATTCGGCC AAAGAGGCCT ACTCAGCTGC AAAAAAGCAT ATTTCTGTG TTTCTGGACT	60
GCACTGTNGT CCTTGCCCTC ACATAGACAC TCAGACACCC TCACAAACAC AGTAGTCTAT	120
AGTTAGGATT AAAATAGGAT CTGAACATTC AAAAGAAAGC TTTGGAAAAA AAGAGCTGGC	180
TGGCCTAAAA ACCTAAATAT ATGATGAAGA TTGTAGGACT GTCTTCCCAA GCCCCATGTT	240
CATGGTGGGG CAATGGTTAT TTGGTTATTT TACTCAATTG GTTACTCTCA TTTGAAATGA	300
GGGAGGGACA TACAGAACTC GAG	323

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCGGCC AAAGAGGCCT AGGCAAATCA GAACTCTTAA GTTGTTTCAT CCTTATTTTA	60
TTCTTAAAT AAAGAATTTC ATTCAAATA CGGATTAAAT TTTTTCCTGG GAAAAACAC	120
ACTGTAAAC ATAATTTTCT ACCTTTTAAA ACGTTTTACA ATTTATCCCA TCTTCTAACA	180
AGTTATGATA CTCATACCTG CCGAGGTTTC TCTAAATTG TCGCTGGTCT TCTTTTCCT	240

CCATTTCCAA GGCTTAAAGA TTTTACCAAT GGTGGATAGT TTCCCTTTTC TTTTGAAGGG	300
AGGTGTTTGG GAACCTGCTG TGGGGCCATC TGAGTTTGCT ATAGAAGCTT TGTCCAGTCC	350
GTCAACTGAG CCGGAGATGT GGACCCGGAG CGGGCGGCCC CTGCTCGAG	409

## (2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCGGCC AAAGAGGCCT ATAAATATAT AATTGACTTA TTTATTAAAT TTAGGAGAAA	60
AAAAAAGTTT TCCTTGACAT TCAGCTCTAT TGGATTTATT TCCATTTAAT TGCATCATGT	120
GTTATGTCTT GGTAAACACT CCATTTCCTG TCTTGGTGGG CATCCTGTCT GTGTACCTGT	180
GCAGTACACT TTAATCATCA AGACTTCAAA GTGCTTTTGA GCTATCAAAT CTGGGGAGAG	240
TCCCATCTAG CATCTTAATA ATTATTTTTC CAAGTTCGTT ATAATTAACCT CCTTTAACCT	300
CATCTCATT AATCAATTTT GTATTATCAT TCTGTTGTT TCTGGAAAGC AGCCAATTGT	360
TCAGCTCTTG AATCAGAATT TTCAAAGACT CACCTCTCTT ACCTGGGCTT GCACATATT	420
GTCCTAAGTA ATTCTCTATC CCTTAAACCT CTGAGCCCTC GAG	463

## (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAATTCGGCC AAAGAGGCCT AATTTTGTA AAAGGAATAT CATTCTTTGA TTTTAGATCT	60
TAGACATCAG GCACTGACAT AGAGCTTAGA TATGTTCTTA AGGTAGCTAA GCCATTATT	120
ATAGGATAGT CAGATAGGAT AGTTCTAGGA TTTATAGACC TTTTCAGATA CTCTTTATCC	180
AGTGAGAGAT GACCTATTTT TATTAAACT TGGGTTTGGT ATCTTGAAT TGGCTTGAAA	240
ATGATTGTG TTTACATGG ATGTGAACGG AAAGTTTGTA TCTCAAATGT TTTACCACCT	300
GAAGGGACAG CTCGAG	316

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGGACATGG AAGTAGGTGA GGTGGGGGA CCTATGAAGA AAAAAAGAGC CTTTCCACTG	60
GGCAGTGAAG TGTGTACACA CACACTGGGG GCAGAGCAGT GTGAAAACAT TCTGCACCAG	120
CACACAAATG ACTTTTGGCA AATCATCTNC CTGATCTGTC GGATGTTACG TCTCTGCAGA	180

ATCTGGAGAA AACCAGAAAA CCCAGCTTGT TTGCCCTCAT TTGGCAGTT TAATTTAGGA	240
ATCACACTGG CTTTACATAA ACTCTTTACC AAAAAAAGT TATTCTGTAT TTTGAAGGCA	300
CAAGTTAACA TGGGCCCAAG GGAAGGAAGC ATTGTATACA ATTACATAAT AGCTACTCTA	360
TTACTTTAAA ACCTAATGGC AGCCTCGGGC AGAAAAGTCA AAAGGGGAGA GAAACCATT	420
CTGTGAAATT ATCTGATGCA ATCATCTCTT TGGAGACATT GTCAGTTGAC AATGGTTCTG	480
CTTTTCTCT CGAG	494

## (2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 507 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAATTCGGCC AAAGAGGCCT ACGGAGCAG TTCATGCAGC ACCTCTACCC ACAGAGAAAA	60
CCTCTTGTGT TGGGAAGGGAT TGATTTGGGG CCATGTACAA GCAAATGGAC AGTGGATTAC	120
CTAAGCCAAG TTGGAGGGAA GAAAGAAGTA AAGATTCATG TTGCTGCAGT TGCACAGATG	180
GACTTCATTA AACTTTACCT TTTGACCAGT TGGTCCAGAG GGCAGCTGAA GAGAAACATA	240
AAGAATTCCT TGTTCAGAG GATGAGAAAT ACTACTTACG GTCACCTTGA GAAGACCTTA	300
GAAAGGATGT TGCAGATATC AGAAAGCAGT TTCCTTTGTT GAAAGGAGAT ATTAAGTTTC	360
CAGAATTCCT CAAAGAGGAA CAGTTCTTTT CCAGTGTTTT TCGAATTAGT TCACCAGGAT	420
TACAACTATG GACTCATTAT GATGTAATGG ATAATTTGTT AATACAAGTG ACAGGAAAAA	480
AGCGTGTGT ACTCTTCAGT CCTCGAG	507

## (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GAATTCGGCC AAAGAGGCCT AGCTTATCCA GTCTAGTAAT TTTTTTGTGTA TGTGTGCACA	60
GCACAAATAG TTACAATAGT TCCCTTTTTT GACATCAAAT TCAACAATAC CTGGCATATA	120
ATTGCTAAAT ACTGTCATCA TTTTCATTAT CATTATCCCC CACATAGTCA TAAATAAGCA	180
CACATGCTAA TCITCAACTC TTCTTCTATT ATTTGCTGCC TTCTTACCTG CGTTAGTGAG	240
AAAGTGCCTT CAAATAGATT GCCAACAGTT ATATGGCTCG AG	282

## (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATTCGGCC AAAGAGGCCT AGTGCAGTAT TCACGTGTAA CTTTAAAGTT TTCAGTACAG	60
TGCTTTTATA CCTTTAATGC AATGTTGTAT TCATTTGGGT ACTATTGTGT AGTATTTAGG	120
ATGTATGCAT GTTTGTTTAT ATGTAAGCTT GGTGGGTGCT TTCGCTTTTG TGCTACCTTT	180
CTTGATTTT TGTACCAGAG ATGTGCTAAA CTGATGAAAT ACATTGAGAA AGTTTCCATC	240
TTATTCTTTT ATATGGGACT GATGATGTGT GTTGGGGTAG ACTGCTCCTG CAGAGTTTGG	300
AAGAAGTCAC CAGCAAAGCC GGCCAATCTC GAG	333

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTCGGCC AAAGAGGCCT AGGTTTCTAG ACTGGAAGAA CAAATGAATG GCTTAAAAAC	60
ATCAAATGAA CATCTTCAAA AGCATGTGGA GGATCTGTTG ACCAAATTAA AAGAGGCCAA	120
GGAACAACAG GCCAGTATGG AAGAGAAATT CCACAATGAA TTAATGCCC ACATAAACT	180
TTCTAATTG TACAAGAGTG CCGCTGATGA CTCAGAAGCA AAGAGCAATG AACTAACCCG	240
GGCAGTAGAG GAACTACACA AACTTTTGAA GGAAGACAAG GAACGCNAGA AAAAAGACGA	300
AGAAAAGGTG AAGGCAGAGG AAGAAATCAA GAAAAAGAA GAGGAAGAAA AAAAGAAACA	360
TCAAGAGGAA GAGAGAAAGA AGCAACTCGA G	391

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAATTCGGCC AAAGAGGCCT AGCTTCTCTG CTTTATTTAT TCATTTATTT TTAATTTTTT	60
GAGATGAAGT CTCGCTCTGT CATCCAGGCT GGAGTGTGGT AGCGCCATCT CAGCTCACTG	120
CAACTTCCAC CTCCCAGGTT CAAGTGCATT GTCTTTTAA TGTCTATGTG AAGGATTCTG	180
AGCTGTACGA GTTCTGCCCC AAATCTGCAC TTGGGCCTCA GGATCAGGCC GCCTCCCAT	240
CAATCTGGTG GATGCCAGTT ATAACCTTTG CCCTGCACCC CATCCACACT GTAGTTCAGA	300
GAAAATCAAC AGTCAGCAAT CATATCACA GCACTCGAG	339

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCGGCC AAAGAGGCCT ACGAGTCAGC ATCTAGACTC AGCTCCTTCT TCCCGCCTGC	60
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CCTCACACAT GCGTGCAATC ACTCTCCTGT CCAGGCTCAT GTCCTTGTGC CCGCTTGCTG	120
CTTTGCCTCC TTGCTTGTTT CTGACTTGCT CACCCACTCT CTGTCATTGT CTTGCTTACT	180
CAGGCTCACC CTATCAACTC GAG	203

## (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCGGCC AAAGAGGCCT AGTTGAATTA TTGCCACATG TTAGGAATGT GGAAGGTTGC	60
TTGGATAAAT GAGAAAAGAA AGAAAAGAAT GCAAGTAATG TCCTGCTGGG GTAGTGCAGT	120
CCTCGAG	127

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 179 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAATTCGGCC AAAGAGGCCT AGATCCCACG AATTTAGGCT CAGAAGCATC GCTCCTCTCC	60
AGCCCTGCAG CTATTCACCA ATATCAGTCC TCGCGGCTCT CCAGGGCTCC CTGCCCTGAC	120
CTCTTCCCTG GGTTTTCTGC CCCAGCCTCC TCCTTCCCCC CCCCCCTATA TCCTCGAG	179

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAATTCGGCC AAAGAGGCCT ACTGGAATCA CTAACTTTG TCTCATTTTT TTTCTTTCC	60
ATCAAATATC AATTTTGGAT TCAGATCCAG TTTTTTCTT TCAATTATTT CTGCCTTTTA	120
AAATAATACT ACCTCCTTCC TCCCACAATT CATTTAGCT TGTTTATGTT CCTTGGGTTT	180
TATATTTTTT CTTCTAGTA TTACAATATA TGCACAAATA TTAGGTTATA AAACCTCCAA	240
TACAACTTTT ACTGCCACTC ACAGGTTTTT CAATTGTTTT CATTTTCATG TACATTAAA	300
TAATGTATAT ATTAGGATA CTCGAG	326

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAATTCGGCC AAAGAGGCCT AAATATGAAA AGCTGTCTAT ATCTACCCAG CCAAACCATC	60
TCCAGCTTTT ACTTTTATTG AGCAAGTATA CGTTATTTAT TTAGTCATCC ATTCATTCAT	120
TCTCATTTT ATTTATTTTT TTTTCAGCTT ATTTCTGCTT TCATCTTAAT TCCTCTCTTA	180
AACCTTTTGG TATCACATTG GTTCTCCCTG ACCTCCACCA CTGTAACCTG ACTTAAGTTA	240
AATGTTTAAT TTATTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	300
TTAGGTAGA GAAGATGTCT CACCATGCTG CCCACTCGAG	340

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAATTCGGCC AAAGAGGCCT ACTTTCTTCC TTATTCTACT TCTCTTTTTT TCTTTGTTC	60
AACATCATGT TTGTGAAAGT TTCATGCATA TCGTTGCAAG TATTGTATT TCATTCATT	120
CTATTGTTGT ATAATGTTAC ATTGCATGAA TATGCAGCAA TTTGTTCTAC TGTAAGGAGC	180
AATAAGGATT TAGTTATTTT CAGGTTGGAC ACAAATAATT TTGCTATGAA GGGTCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAATTCGGCC AAAGAGGCCT ATAACTATAT AGCCTAGAAT TTTTCCTATT CTGTTATTAA	60
GCCTCTATCA CTATTCTTTG ATTCTAGGTT TTATAATCCA TTCTTTTTTA TAACAACCTG	120
TTCTTGTTT ACTTTTCCCT ATTTTGTGTT TATACCCATC TATTCTTTT TAGGATCTAT	180
TCTCCACTTT TAACTTTGAG GATTCTAAAA TACTTACTTT AAAGTTATTT TTAAGTTGTT	240
CTATTTTGT TTTTGTGAG AGCGAATTG CCTTTTTTAT TTGGCTGTTT TACCATGCTT	300
TTTGGAATTT TGTTTGTAG GCTTCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAATTCGGCC	TTCATGGCCT	ACTCTACTCC	AAGTAGGAAA	AGGCCAGGAG	GTCCTGTAA	60
AGGATGCACT	CAGAGCCCGG	GCTCCCTAAC	GTATGAGAGT	GCTAACCAGC	AGGTGTAGAC	120
TTTTCAGGAG	TGAAGAATGA	GGCAGGCATT	CCAAACCTGG	ACCTTCATCA	CCTTTTGT	180
CATCTCAAGA	CAATTCTGAG	GGACTGTTTT	GGAGCGTGTC	TGGAAGGTGA	ACGTTGAAGA	240
AGAGTGTGGG	CTTTGATGTG	ACTCAGTTGA	ATACTCGAG			279

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCTCAT	GAAACTCTCA	GCGGAAAGCT	ACAAGGAAAC	ACAGATGGTG	AAGATTAAAG	60
AGGAACCCAT	GGAGTTGAC	ATCCAGGACT	CCATGTCTC	GATATCACC	AGCCGGAATG	120
TTGGCTACAG	CACTTTAATC	GGGCGAGAGA	AAACCGAACC	CTTACAGAAG	ATGCCAGAGG	180
GCAGAGTACC	CCCAGAGAGA	AACCTCTTCA	GTCAGGATAT	CTCTGTGAAA	ATGGCTTCCG	240
AGCTCCTCTT	TCAACTGTCA	GAAAAAGTGA	GCAAAGAGCA	CAATCATACA	AAAGAAAACA	300
CCATCCGGAC	CAATCTCGAG					320

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTCGGCC	TTCATGGCCT	AGAGCAACAT	AGTGAGACCT	CATCTCTACA	AAAAATAAAG	60
AGAAAATTAG	TTGGGGGTGG	TGGCGTGCAC	CTATAGTCCC	AGCTACTCAG	GAGGTTGAGG	120
TGGGAGGATC	ACTTGAGCCC	AGGAGTTTGA	GGCTGCAGTG	AGCTGTGGTC	ATGCCACTGC	180
ACTCTAGCCT	GAGTGACAGA	GCAAGATCCT	GTCTCAAAAA	ATAAAGTAAA	ATAAAATAAT	240
CAGTCAACAA	CAGTGATTG	TCTTCAAGCT	GCCCTCCTCT	TGGGCTCTCA	AGGCAGTTTG	300
TGAAGTGTCT	AGGATAGGAA	TTTCCAGAA	GGGCTTGCTC	GAG		343

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGAAGATGTG	CCAAAGTTCA	GAAAACATAA	TCTTATCTGA	TCAGATTAAA	GATCACAAC	60
CCAGTGAAGC	CAGATTTTCT	TCAAAGAATA	TTAAGGATTT	GCGATTAGCA	TCAGATAATG	120
TAAGCATTGA	TCAGTTTTTG	AGAAAAAGAC	ATGAACCTGA	ATCTGTTAGT	TCTGATGTTA	180
GCGAGCAAGG	CAGTATTCAT	TTGGAACCTC	TGACTCCATC	CGAGGTACTT	GAGTATGAAG	240
CCACAGAGAT	TCTTCAGAAA	GGTAGTGGTG	ATCCTTCAGC	CAAGACTGAT	GAAGTAGTGT	300
CTGATCAAAC	AGATGACATT	CCTGGAGGAA	ATAACCCNA	CACTCTCGAG		350

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GAATTCGGCC	TTCATGGCCT	ACTCGCGGTC	TGTTAGTAGT	ATAGTGATGC	CAGCAGCTAG	60
GACTGGGAGA	GATAGGAGAA	GTAGGACTGC	TGTGATTAGG	ACGGATCAGA	CGAAGAGGGG	120
CGTTTGGTAT	TGGGTTATGG	CAGGGGGTTT	TATATTGATA	ATTGTTGTGA	TGAAATTGAT	180
GGCCCCTAAG	ATAGAGGAGA	CACCTGCTAG	GTGTAAGGAG	AAGATGGTTA	GGTCTACGGA	240
GGCTCCAGGG	TGGGATGAGC	GGGCCAAGAT	CGATGATCCC	ACAGACTCCA	AGCCTGAGGA	300
CTGGGACAAG	CCCGAGCATA	TCCCTGACCC	TGATGCTAAG	AAGCCCGAGG	ACTGGGATGA	360
AGAGATGGAC	GGAGAGTGGG	AACCCCCAGT	GATTGAGAAC	CCTGAGTACA	AGGGTGAGTG	420
GAAGCCCCGG	CAGCGTCTCG	AG				442

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAATTCGGCC	TTCATGGCCT	ACAGAAAGTA	AGTTGGAACC	ATGTAAGAAA	AAAAGACACA	60
AATAAACTA	GGAAAGTGGC	ATGGAGCTAG	GCGTGAAGTT	GCTGCTCAGT	TTACATGTAT	120
GAAGTTCTGT	GTGGACTTAA	GCTCCTACTT	CAGTCATTTA	TTGTATGACT	TGGACAAGTT	180
GCCAAACATC	TCTAATATTC	ATTCATATTT	GTAGGGTAAA	AGGATGAGTA	ATATGTATCT	240
TTAGTGTATA	AAACATTTAC	AGACAACTCG	AG			272

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAATTCGGCC	TTCATGGCCT	AAGACACCAG	CGAGCCCAGG	CAGGTAATGG	AAGCAACTGT	60
AGCTGACTGG	ACCTAAGAAG	CAGTGGCACG	GGTGCCAGGC	ACCCCAGCTG	ACCTGCCTTG	120
GTGCTCAGAG	CAGCAGGGCT	GGCCATGGTC	AGGGAGTCTG	GGGAGGTCAT	GCTCTGTCCA	180
CAGGGTTCTA	GCCAGCTTCT	GCCAAATTGT	CTGTTTTTTC	TCAAGAGAAG	CTGGGAAGGC	240
CAGTTGTGGT	GTCTCATACC	TGCAATCATA	GCACTATGGG	AGGACTCGAG		290

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAATTCGGCC	TTCATGGCCT	ATGAAAATTT	GGAAGAAGAA	TCCAATGAAA	GTGGTAGCCC	60
TTTTGACCCT	GTTTTTGAAG	TTGAACCTAA	TCTCTAACGA	TAACCCAGAG	GAACATGTAC	120
TGAAGGTAAT	TCCTGAGGAT	GCTTCAGAAT	CTGAGGAGAA	GCTAGACCAA	AAAGAGGATG	180
GTTCAAAATA	CGAAACTATT	CATTTGACTG	AGGAACCAAC	CAAACTAATG	CACAATGCAT	240
CTGATAGTGA	GGTTGACCAA	GACGATGTTG	TTGAGTGGAA	AGACGGTGCT	TCTCCATCTG	300
AGAGTGGGCC	TGGATCCCAA	CTCGAG				326

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTCGGCC	TTCATGGCCT	ATGGCAATGG	TGGTCGTGGT	GCTGGGTGGG	ATGNGGTCTT	60
CATCCTCTTC	CTCCAGGAAG	GATGCCTCTG	GGATATGGCT	GAAGGCCTCT	GGGTGCAGCC	120
TGGCCAGTTT	CCCTTTCAGC	GTCCTGATAC	GGCGGAAGAT	GATGTCCAGG	TCCCGTTTCA	180
TCTCTACTAG	GGTCCTCGTG	TGGTGCAGGA	AGCGTTCGCT	CATCTGCTGC	AGGCGGGCAT	240
TGGACAGGTT	GTTGAAGTTG	AGCAGCATCT	CATTGGTCTT	CTCAAAGCGG	TCCAGCATGT	300
TCTTCTGGGA	CAGGATGATG	GCGTTGACAT	CATCTGTGTT	CACCATGCTC	AGGATGCGGC	360
CGCAGAAGAC	CCTCGAG					377

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GAATTCGGCC	TTCATGGCCT	ACATGACACC	ACCTGAACGT	CTCTTCCTCC	CAAGGGTGTG	60
TGGCACCAACC	CTACACCTCC	TCCTTCTGGG	GCTGCTGCTG	GTTCTGCTGC	CTGGGGCCCA	120

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GGGGCTCCCT GGTGTTGGCC TCACACCTTC AGCTGCCCAG ACTGCCCGTC AGCACCCCAA 180
GATGCATCTT GCCCAGAGCA ACCTCAAACC TGCTGCTCAC CTCATTGGAG ACCCCAGCAA 240
GCAGAACTCA CTGCTCTGGA GAGCAAACAC GGACCGTGCC TTCCTCCAGG ATGGTTTCTC 300
CTTGAGCAAC AATTCTCTCC TGGTCCCCAC CAGTGGCATC TACTTCGTCT ACTCCCAGGT 360
GGTCTTCTCT GGGAAAGCCT ACTCTCCCAA GGCCACCTCC TCCCCACTCT ACCTGGCCCA 420
TGAGGTCCAG CTCTTCTCCT CCCAGTACCC CTTCATGTG CCTCTCCTCA GCTCCCAGAA 480
GATGGTGTAT CCAGGGCTGC AGGAACCCTG GCTGCACTCG ATGTACCAGG GGGCTGCGTT 540
CCAGCTCACC CAGGGAGACC AGCTATCCAC CCACACAGAT GGCATCCCCC ACGCACTCGA 600
G 601

```

## (2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

GAATTCGGCC TTCATGGCCT ATTTTTTTT TTTTATCAA AAGTTTGTTC TATTTTCAAT 60
ACAAGATAAA TACCATGCTT GTTACTAGTG CAGTTCTCGA G 101

```

## (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

GAATTCGGCC TTCATGGCCT ACAGAAATGG AGGCATGATG AAGACTCTGC TGCTGTTTGT 60
GGGGCTGCTG CTGACCTGGG AGAGTGGGCA GGTCTGGGG GACCAGACGG TCTCAGACAA 120
TGAGCTCCAG GAAATGTCCA ATCAGGGAAG TAAGTACGTC AATAAGGAAA TTCAAATGC 180
TGTC AACGGG GTGAAACAGA TAAAGACTCT CATAGAAAAA ACAAACGAAG AGCGCAAGAC 240
ACTGCTCAGC AACCTAGAAG AAGCCAAGAA GAAGAAAGAG GATGCCCTAA ATGAGACCAG 300
GGAATCAGAG ACAAAGCTGA AGGAGCTCCC AGGAGTGTGC AATGAGACCA TGATGGCCCT 360
CTGGGAAGAG TGTAAGCCCT GCCTGAAACA GACCTGCATG AAGTTCTACG CACGCGTCTG 420
CAGAAGTGGC TCAGGCCTGG TTGGCCGCCA GCTTGAGGAG TTCTGAACC AGAGCTCGCC 480
CTTCTACTTC TGGATGAATG GTGACACTCG AG 512

```

## (2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAATTCGGCC	TTCATGGCCT	AAATTATTAA	AGGTGACAGT	ACACAGGAAA	CATTACAATT	60
GAACAATGCC	TCAGCTATAC	ATTTACATCA	GATTATTGGG	TGCCTATTTG	TTCATCATT	120
CTCGTGTTCA	AGGACAGAAT	CTGGATAGTA	TGCTTCATGG	CACTGGGATG	AAATCAGACT	180
CCGACCAGAA	AAAGTCAGAA	AATGGAGTAA	CCTTAGCACC	AGAGGATACC	TGCTCTTTT	240
TAAAGTGCTA	TTGCTCAGGG	CACTGTCCAG	ATGATGCTAT	TAATAACACA	TGCATAACTA	300
ATGGACATTG	CTTTGCCATC	ATAGAAGAAG	ATGACCAGGG	AGAAACCACA	TTAGCTTCAG	360
GGTGATGAA	ATATGAAGGA	TCTGATTTTC	AGTGCAAAGA	TTCTCCAAAA	GCCCAGCTAC	420
GCCGGACAAT	AGAATGTTGT	CGGACCAATT	TATGTAACCA	GTATTTGCAA	CCCACACCGC	480
TCGAG						485

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC	TTCATGGCCT	ACACACATTG	TGAGCTGTAT	ACGTTAACCC	AAAGTCTGCA	60
TTCAAAGTGG	AATTATAACT	GGGCAGTGAA	TGAGTTGCTC	AGTCCATCTA	TTAACCATAC	120
TCTTTTAGGC	TTTTTATTGC	CTCTAATTGT	TGTAATAATT	AACATTTTCC	CAGGAAGTTG	180
TTTACAGAA	GAAGGGGCCT	TAGCGGCTTT	CAACTCTTTA	GAGATAAGTT	CAACTTTGTG	240
GATTGACCAC	AGCACATCTT	GTTTAGTAGT	GAGCGGGAGC	CATATGAATC	CTCTAGAGAC	300
ACAGCCGTGT	CTGAGATGGA	CATTGCCAAC	ACAGCTCGAG			340

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTCGGNCCTC	ATGGCCTACT	CTCATAAAAA	TATTCAAAGA	TCAACCCCAA	ACGTGCCTGC	60
ANTTTGGACA	ATGTNAGCTA	AAGCTATAAA	TGGAACAGCA	GTGGTCATGG	ATGATAAAGA	120
TCAATTATTT	CACCCAATTC	CAGAGTCTGA	TGTGAATGCT	ACACAGGGAG	AAAATCAGCC	180
AGATCTAGAG	GATCTGAAGA	TCAAAATAAT	GCTGGGAATC	TCGTTGANGA	CCCTCCTCCT	240
CTTTGTGGTC	CNTCTTGGCA	TTCTGTAGTG	CTACACTGTA	CAAAGTGGAG	CATCTGAGTT	300
ATAAAAGTTG	TGAGAGTCAG	TACTCTGTCA	ACCCAGAGCT	GGCCACGATG	TCTTACTTTC	360
ATCCATCAGA	AGGTGTTTCA	GATACATCCT	TTTCCAAGAG	TGCAGAGAGC	AGCACATTTT	420
TGGGTACCAC	TTCTTCAGAT	ATGAGAAGAT	CAGGCACAAG	AACATCAGAA	TCTAAGATAA	480
TGACGGATAT	CATTTCATA	GGCTCAGATA	ATGAGATGCA	TGAAACACTC	GAG	533

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC	AAAGAGGCCT	AGAAAATAGA	AAATCAGGTA	GCTATGTCAT	TTTATAAGCA	60
TCAGTCCTCA	CCAGATTTGT	CAAGTGAAGA	AAGTGAAACA	GAAAAGGAAA	TTAAAAGGAA	120
AGCTGAAGTT	AAGAAAACCA	AAGCAGGAAA	CACCAAAGAA	GCAGTGGTTC	ACCTGAGAAA	180
GAGCACAAGA	AACACAAGTA	ATATTCCAGT	GATTTTGGAA	CCTGAAACTG	AAGAAAGTGA	240
AACAGAAAAG	GAAATTAAAA	GGAAAGCTGA	AGTTAAGAAA	ACCAAAGCAG	GAAACACCAA	300
AGAAGCAGTG	GTTACCTGA	GAAAGAGCAC	AAGAAACACC	CTCGAG		346

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC	AAAGAGGCCT	AGGCAGGTAT	TCTTTGCTTT	GGGAAATTCT	TCTTTCTGTC	60
CTCCCTTCCC	TCACITTTTC	CAAATTCTGG	GCACAACAGC	AGCTCTCTCT	CTTCTGTGGC	120
AGGTGTGCAT	CCTATTGGCT	GGCTGGTATT	TCTGTGTTTT	TTTCCCCCTT	ATTCTTTTTA	180
AATGGGGGTG	GGGTATAAAA	AATATGTGTA	TGGGGTACAT	GCAATAATGT	TGTAATGTTT	240
CTTGTTGTTT	AATGGATAAT	TAATTGCAAA	ATAATTGTTT	TAAITATAAC	ATGTTTGAGT	300
AAATGCTAAA	TTAGTATTTT	TTTCTAATAT	AATAATGAAT	TTGAAATCTA	GCATTCTCTG	360
AACAATGTGT	CTATGTTTGT	CTGTCTGTGT	CTGTCTAATA	GTAATTAATA	TCTGTGGTCC	420
GCACCCACTC	GAG					433

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC	AAAGAGGCCT	AAGCAAAGCT	TAGCTTACGG	GGAAAAAAA	AAAAAAA	60
AAGTAGAGCT	TNCCTTGAAT	CTGGAGAAAT	TAAGCACACA	GGTGTCTGTC	AATATTAGTT	120
AAGAGACTAC	TGCACCCATC	ATACTGTAGC	TTAAGACAGT	TTCTTCTTTT	AGTTTTTTCT	180
AAAATGTCTC	CATGTCTGTG	TTATGCCACA	AATAACACAG	CCTTGGTTAA	CTTTTGACT	240
AAAAAAAATC	AACTTATTGG	CCAAGCATGG	TGGCTTACAC	CTATGATTGT	AGCACTTTGG	300
ATAGGTCTCG	AG					312

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC AAAGAGGCCT AATTTTCCTA ACTGTGTGCT GCCTTTTGGG TTAATTAGAA	60
TTGTAGCATT TCGTTTGTAT TATTTTTTTG GCTCTTTAGC TGTTCCTCA CATTTTAA	120
AATGGTAACT CTAGGATTA TAATATGCAT CTTTAATTTA TCAAAGTCTG TTTTACTAC	180
TTCGTGTAAA ATAAACGAAC CTTGCATTTA TAGTTACATT TATTCCTCTC ATCTCGAG	238

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC AAAGAGGCCT ACTCAAAAGT AGATGAGCAA TTGGTCAGAA TTGTTAGAGG	60
ATATTATTTG AGCTAAATGT TTCCTCTCTC TGTTTCAGTG GTGTATGTGC AAGTGTGTGT	120
ATATGTTTTT TGTTGGGGAC AGTTTCAGGT AGATGGTATG AAGAGGCAGC AGGAGACTCT	180
CGAG	184

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCGGCC TTCATGGCCT AATTTTCTAA AACCTGGAGA CAAACCACAT AAATACAAAA	60
CAAGTCTGCT TCTTCAAAAT TCTGCTGGTG AGAACTCAGA TATCAGTGAT CTTATTAGCT	120
TTTTCAACAAG CCAGAACATA ATGGTGACGA TGATTAATGA CAGTGACTAT GTATCCGTGG	180
CTCCCCATAG TGCGGCTTTA AATGTGATGC ATTCAGAAAA GGACTATGTT TTTGCAGCTG	240
TTTTCAACAG TACTATGGTT TATCTTTAC CTATATTAGT GAATATCATT AGTAACTACT	300
ATCTTTATCA TTTAAATGTG ACTGAAACCA TCCAGCTCGA G	341

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GAATTATGCT GTGCTGTTTT CCTGGACACT CAGAATCAAA CAGGCCTTCC ACCCCATCCC	60
ATCATGTTGA ATTACAAAGT ATTTTGAGCA TCGTTTGGTT TGTTTCTTTC CACCCATACC	120
TGTGTAGGGC AGCGGTAGCA GTCTTCAACA ATGCATCCTC TTGGACAATG CATGTGAATA	180

TCTCTCTTTC AAATTCTGTT TCACATAGTC ATTTCTCATG TTCTGTTGGA GACCCCCAAA 240  
 AAATTCATTC CACACTGTCA TCCCTTTGTC CTAACCAGAA TCTCGAG 287

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC TTCATGGCCT AATGTATGGT AGACAATTTT TTTTAAAGAC ACAGAGATAA 60  
 ACGTTTTCTT GCTTTGGTTA CCTTTCCTTT CCCCTTTAAA AGGAATTAGC TATAGAAGCTG 120  
 CTTTGTAAGG ATGCTTCTTG ATATTTTACT TTTGTTTCCTT TTCCCTAATC ATTCCCTTTT 180  
 CACCCCACTC CTCGAG 196

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC TTCATGGCCT AGTGATTGGG TGCAGAGGAA ACAGGAACCA GAGAAGGGTC 60  
 ATCTCAGCTG CCTGTCCAC TCCTATGCT TGGTGTTACC TGCGCCATAG TCTCGAG 117

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GAATTCGGCC TTCATGGCCT AGTAAGTGCT CTGAGTATAT TAGGAAAAGG AAATCTTATA 60  
 CATAAAAATC AAAGCTGTTG CTAATTTTTC CACTAGTGAG TCAGTCTATT AACATTACTC 120  
 ATGGTAGGTT TTGCCATACA GAATTTTAAT TTTTATATAT TA'TTTTGGC TTTGTTATTA 180  
 TGCTTAGAAG TCCATGGGGA CCCAAAGATC AGAAAAGATT CATCTGTACT CGAG 234

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCGGCC	TTCATGGCCT	ACGGAACGAA	CATTGGCTCG	GCGGTGGTGA	TGCTAATTCC	60
CACTGTCATG	TTCACAGTGA	TGGCCGTCTT	TTCCTTCATC	GCCCTCAGCA	TGGTTCATAA	120
ATTTTACCGG	GGAAGTGGG	GGAGTTTCAG	CAAAGCTCAG	GAGGAGTGA	CCACAGGGGC	180
CTGGAAGAAT	CCACATGTGC	AGCAGGCAGC	CCAGAACGCA	GCCATGGGGG	CAGCCCAGGG	240
TGCCATGAAT	CAGCCAAGAC	TCGAG				255

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTTGCCA	CACCATGAAG	CTCTTGTTGGC	AGGTAAGTGT	GCACCACCAC	ACCTGGAATG	60
CCATCCTGCT	CCGTTTCGTC	TACCTCACGG	CGCAAGTGTG	GATTCTGTGT	GCAGCCATCG	120
CTGCTGCCGC	CTCAGCCGGG	CCCCAGAACT	GCCCCTCCGT	CTGCTCGTGC	AGTAACCAGT	180
TCAGCAAGGT	GGTGTGCACG	CGCCGGGGCC	TCTCCGAGGT	CCCGCAGGGT	ATTCCCTCGA	240
ACACCCGGTT	CCTCGAG					257

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC	TTCATGGCCT	AGGAAAGATT	CGTGTTTTAC	TTTAATAAAC	CTGAAAGAAC	60
TGTCGTTTTT	CACTGCCTAT	AGGACCACTA	CAAAGCCGCA	AAGAAAAATT	AGACTTGTTT	120
CATTTTATAA	CAACAACAAC	TGCTACTACT	GCTACTAGTT	AGATACCGTT	TGCTCATTTA	180
TAACAATCTC	AGTTGGTAGG	ATGAAGCTTA	AACACTTGGC	ATTCATCGTC	TTTTTCAGTC	240
CTCTCGAG						248

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCGGCC	TTCATGGCCT	ACTGTCTTTT	CATGCAGATT	TCATATTGTC	TTTGTCTTT	60
TCATTGCTTC	TTGACCTTCC	TGGCAGGTGT	CGCTCAGTTT	CTTCCTGTTT	CCCTTCCTGT	120
CCTCTCCACA	CCTGCTATCC	CGTCCCACTC	CCATCTACCT	CCCGGGAAGC	CAGCCCTGCA	180
TGCTGAGTTT	GTGACCTGCT	TCATTCCCAT	TTCATTCTA	GAGGGTTTAG	AGGTGACCTG	240
GAACCGTTCC	CTTCCCTCT	CCTACCCCT	CCTCTGCAAC	ACCAAGAGGC	CTGGAGGGGC	300
AGACAGAAAG	CAGCCAGCCA	CGCGGGAAG	TCTCGAG			337

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCGGCC	TTCATGGCCT	AACCTATTTC	TTTGTGTGAT	TGCCTGTCTT	TCTTTTCTTT	60
TCCTTCCCTC	CCTCCCTCCT	TCCCTTCCTT	CCTTCCTTCT	GTAGAGATGA	GGTTTCACCA	120
TGTGGCCAGG	TTGGTCCTGA	GCTTAAGTGG	TCCTCGCACC	TCAGCCTGGC	AAACTGCTGG	180
GATTACAGGT	GTGGGCCATC	ACGCCTGGCC	TTACAGTAAA	TTCTTGATAA	ACAACCCAGC	240
AACACACCTC	GAG					253

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GAATTCGGCC	TTCATGGCCT	AGGACGGGGG	ACTCAGGTTC	TACACTGGAA	CCTGGGGTCA	60
TGTATCATGT	ACCAGGTGGG	GAGAAGTGTA	GCAAATCTCA	GTGCCAATT	GAGGGGAAGC	120
CAGTCATTCC	AGGAGAAGAG	CTGAGGGGAA	AGAGCTGTTG	ACTTTCATAA	TGCAGTCTTA	180
ATTATCCAGT	CACCCTCCTG	CCACATGGCA	GAAGCCAGGT	GGCAGTGATG	GTGGTGGGGG	240
AAACAAAACA	CACAGTCTCT	GGCAAGCCCC	ACCGGGAAG	GAGGGCTCAG	AAGGCGTAGC	300
GGGTCCGGAT	ATCCTCGAG					319

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GAATTCGGCC	TTCATGGCCT	ACAATAAAAG	CCCATAGGGA	AGAGAGAGAG	GATATAGGGA	60
AACAGATCA	GATGTGTAAT	ATACTTGGCA	CAGCGAAAAA	ATGGATTAA	AAGCAAAAA	120
TGGAGGTCCA	GGTAGATGTA	ATTCACACAG	ACTGAAAGTG	AGTTCGGGCT	TGTGTAAAC	180

ACATGAGATT GGATTTGACC CCTTGGCTCT CAAGTGTCCT CTTAGATCTA GAACTGCTCC	240
TTGGTGGCCA TTAGATCGAG TCAGTTTGA TCTGCATCAC TTAGTTATTG GGAATTTCTT	300
TGTTGGAAAC AGGAAAATTT TTTTAGATTA TTTGGCGTAC GGCTCGAG	348

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTCGGCC TTCATGGCCT AGGCACAGTG AAACCCGTGG AAATTCAAAG GTGAGCAGGA	60
CAGTGGGTCC TGTATCTTGA TCTTTACGGA TCTTTCTCTT CTTGAATCCT CACAGCACCC	120
ATTTTATAGA CAGGAAGACT GAGGCCCGAA AGTTCTGTCT GACTCTGAGC CTGGCCTCTT	180
TGCTGCCTCC CGTTGTCCTG TGAGGCTGTG TGGTCACAGC ACCCAGGACT TGAGAGGAGT	240
GAAGTTCTTC CTCACCCCGC AAAGGCTTCA TGAGCCCTAC TGTGTGCCAG GCCAGCCCTG	300
CTCAGTCTGG GGCATAAAC ACAGGGCAGA TTCTGAAAGC CTGTGTGAGG GAAGTTCTAG	360
GCCTGCAGGA GCTGAGAGGA GACCCTGGAG AGGAAGGGAG TCAGGGCCAG CTTCTCTGAG	420

## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCGGCC TTCATGCCTA AGCTGATGGA GACTGTAAAT GAACCAGAAA CAGGTGAAGT	60
GAGCAAAGAT GCAATCATTG TAAAGCAGGA GAAAAATAAT GAATATTGCC TTCAGGATAT	120
TGATGATAAA TTGTCAGAAT CAGCAGAGGA TGATGGTGAA GATGATACCA ATGATGAAGA	180
TGATGATGAA GATAGTAACC CTAAAAAGAA TACTCAGGCC CCACTAGAGT TAATGGCAGA	240
ATTTCTGAGA GCAGAAATGG CCCGAGAGTA CCAGCTGGCA AAAAAATTAT GTCAGATGAT	300
CCTAATCTAT GAACCAGAAA ATCTGAGGC CAAGGAGTTT TTCACACTTA TTGAAGAAAT	360
GTTGCTGATG GAGAAAACTC AGAATCATGA GCAAGACGGT GAAAACAGTG ATGAAGACAG	420
CAGCGGGCTC GAG	433

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAATTCGGCC TTCATGGTCT ACAAATCAA CTGCAAGCAG CCATCATCAG TTTGGAAGAA	60
GCCTTGGGAA GCCTTCAAAG AAAAACCTCG GTATCCACCA AGTCAGGCTC AAGCAGCTCT	120

TCAAGACAGT	CCCCCTGAAG	AGTACTCCTA	TAAGAAATCA	ATAAGAAACC	TGTTTAAAAA	180
CATTCTTTT	GTCCTTCTGT	TGATCACTTA	TGGTATCATG	ACTGGTGCCT	TTTATTTCAGT	240
CTCAACGTTA	TTAAATCAAA	TGATATTGAC	ACAACGCGAG			280

## (2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAATTCGGCC	TTCATGGCCT	ACGCGAGCGG	CAGGTGTGCA	CAGGAGGTTC	TCCAATTGT	60
NCTCTGAAC	CGCGGTCAGG	ATGGTTTCT	CTGTCAGGCA	GTGTGGCCAT	GTGGGCAGAA	120
CTGAAGAAG	TTTACTGACG	TTCAAGATAT	TCCTTGTCAT	CATTGTCTT	CATGTCGTT	180
TGGTAACAT	CCTGGAAGAA	GATACTGATA	ATTCCAGTTT	GTCAACACCA	CCTGCTAAAT	240
TATCTGTTG	CAGTTTGGCC	CCCTCCTCCA	ATGGTACTCC	AGAGGTTGAA	ACAACAAGCC	300
TCAATGATG	TACTTTAAGC	TTACTCCCTT	CAAAACGAAAC	AGAAAAAACT	AAAATCACTA	360
TAGTAAAAAC	CTTCAATGCA	TCAGGCGTCA	ATCTCGAG			398

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC	TTCATGGCCT	AGGGCGATGG	TGGGCAGAGG	ATCCTTAGTG	CTCAGTCGGG	60
CTCCACCAGA	ACCACGGA	TGAAGGAGAA	GAGACTCTCG	GTTCCAGGTA	GCAGAAAACG	120
TGGAGTTTG	GACACAGATC	CTCCTGGCCA	GAGAAGGATG	CTTGAGAATC	TGAGATTTAC	180
ACAGCTGTAT	TAGGTTGTCC	ACGATGACCG	GGCAGTAGGT	CTCTCTCTG	GGGATTTCTT	240
CAGTGGTCTG	CCAGAGACGG	GCGTGAGAGA	TCACATTCAG	AACGCACTCG	TCTTGGTTCT	300
CTATGTGGTT	CCTTGGATCA	TCAACAAGGC	TAAGCACTTT	CTCGGGAAGG	CCTTCTATTA	360
ACTTGGTCTT	GGTGAGCCAG	AGGGCCTGCT	TTACACCCTC	GAG		403

## (2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC	TTCATGGCCT	ACTCCATTTT	TCGAATGGCT	TATTTAGGCC	CAGCTCTTGC	60
GTTTGCATTG	TCCCTTCAGG	CCCAGAACTT	TCTCACGTCA	TCGTCAACAG	GCCTAGCTTC	120
TGCATCTGGT	CAGCCTTTTA	AGGCCAGCT	TTGCCTCAT	AAACTCAGCT	CCTGTTTAAT	180

GGCGGCCTCC CGGGTCCAC TCGAG

205

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC AAAGAGGCCT AGTTTTATTA CTTTGGTTAA GACATCAGTT ATTTTAGTCT 60  
TTGATAATTC ATTATCTAGA TAATGGTTAC TTTGTATTGT CTGTTTCTCG AG 112

## (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC AAAGAGGCCT ACACAGAGCC CTCAGTACT TTAAATTCTT CTAAATTGG 60  
TTGTTTCATGT TAATTAAATT ATTATTATTT TTTTGTGAGA CGGAACCTGA G 111

## (2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 324 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC AAAGAGGCCT AAAGATGTTT TCCATGAGGA TCGTCTGCCT GGTCTAAGT 60  
GTGGTGGGCA CAGCATGGAC TGCAGATAGT GGTGAAGGTG ACTTTCTAGC TGAAGGAGGA 120  
GGCGTGCGTG GCCCAAGGGT TGTGAAAGA CATCAATCTG CCTGCAAGA TTCAGACTGG 180  
CCCTTCTGCT CTGATGAAGA CTGGAACCTAC AAATGCCCTT CTGGCTGCAG GATGAAAGGG 240  
TTGATTGATG AAGTCAATCA AGATTTTACA AACAGAATAA ATAAGCTCAA AAATTCATA 300  
TTTGAATATC AGAAGAATCT CGAG 324

## (2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
GAATTCGGCC AAAGAGGCCT AGGTCCAGAA ACATTTAAAA AAAAAAAAAA GGGGGCTTGA    60
GAAAAGGGCT TCCAGTGCCA GGCAGAAATA TGTTTTCTT AATAGGGC    108
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
GAATTCGGCC AAAGAGGCCT ATGAAAACGT GGATTGCTT TGTAACTTG AGAATACATT    60
TTGTTGCCAA CAAAAGAGA GAAGAGAAGA GGAAGATATT GAAGAGAAGA AATCGATTAA    120
GAAAAAAATT AAAGAACTTA AGTTTTAGA TTCTAAAAAT GCCCAGAACC TTGTAAAGTA    180
TCATATTCCA ATACCATTCA AAGACAGTGG AAATATTTCT TTAAATGATT TCATTTTCTT    240
TAAGACCGAT TATTCATTAT TTGCTATTTT CATTTTGTTA TTATATGCAT GATAAATTCA    300
CAGATACTCT CGAG    314
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
GAATTCGGCC AAAGAGGCCT AGGGTAAGAC TAGAGTGTTT TAAATCATCA ATAAAAAGTG    60
GAGAAAACAA AGGTTATTCA GCGATTGAAT TCTAGACCTG CCTCGAGCCC TGCCTTTCCT    120
TTACTTTTAC TTTTTTTTTT TTTTCTTG GAAGAGAGAA GAACAGAGTG TTCGATTNTG    180
CCCTATTTAT GTTTNTANTC GGAACAAAC GTTGGTTGTG TGTGTGTGTG TTTTCTTGTG    240
TTGGTTTTTT AAAGAAATGG GNAGAAGAAA AAAAAAATTC TCCGCCCTT TCCTCGATCT    300
CGCTCCCCC TTCGGTTCTT TCGACCGGTC CCCCTCAAC CTGCCTCGAG    350
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
GAATTCGGCC AAAGAGGCCT AGAGAGTCTG GATGACAAGC AAAGCTCAAT CTCAAAACAA    60
```

TAATTTTAA AGTAATGATT ATCTTAACCA TTCTTAAATC CTTCTGTCTA GTAGGAATCT 120  
TATTCATGGG AGTGTCTGGA AAAGGGACAA AGAGCGGCTA TCTCGAG 167

## (2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC AAAGAGGCCT AGTGTTCAC AAAAGAATTG GAAACCATAG TCCTGAACTC 60  
TCCCTAAGTA GTATAAGCTT TAAATAGCAC TCAATCCATA TTAAGTCTTC TTAGTGTAGC 120  
ATGGTTGCTC TCATGCGTCT TTCTTATGTT TTAATGGTG TAAATTTTAG TCGTTTGTC 180  
TTCAGAAGTG GCTTTGCAA TACAAAATAT CTCGAG 216

## (2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TAATCTTTAC TGGTGAAAAG GATGGAAAAA TAAATCAACA AATGCAACCA GTTTGTGAGA 60  
AAAAAAAAAA AAAAAAANC CGAAAAAAA AAAAAAACA CCTGAATGCG GAAGAGCTCG 120  
GCTCCCGTTT AGCATTTTGT ACTTAAGGAA ATAAAAAACC AACAAAGGAT CTCACATTTT 180  
CTTAAAAAGT GAAGATTGCT GTATACTATT TATTCAACTT ATAATTATG TTAATCCTTG 240  
ATCTTTGCTT TTGTGTCATG CAAAGCATTT ATTTAATAAA GTTATGCATT CAGTTCTCGA 300  
G 301

## (2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC AAAGAGGCCT AGTCTCTGTT AATCCTACTC TGCTTTAGCC AGAATAGCCT 60  
AGTATTTTAT TTCTATTTTA TATATTGAGA TTTCTTCTAA CATTTCTTTT GATAAAAATC 120  
TTCTGCTTTT TGAAAAGTGG TATGTATCAT ATTTTATGT TTCTGGTGTG TCTCGAG 177

## (2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCGGCC	AAAGAGNCGT	AGGGAAAGAT	TTCAGCTATT	AATCAACTGG	AGGAAATTCA	60
AAGCCAGCTG	GCTTCTCGGG	AAATGGATGT	CACAAAGGTG	TGTGGAGAAA	TGCGCTATCA	120
GCTGAATAAA	ACCAACATGG	AGAAGGATGA	GGCAGAAAAG	GAGCACAGAG	AGTTCAGAGC	180
AAAACTAAC	AGGGATNTTG	AAATTAAAGA	TCAGGAAATA	GAGAAATTGA	GAATAGAACT	240
GGATGAAAGC	AAACAACACT	TGGAACAGGA	GCAGCAGAAG	GCANCCCTGG	CCAGAGAGGA	300
GATTCTCGAG						310

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTGGCCTTG	GGTCAAGATT	CGCACCATGG	TGGGCACAAA	CCCAGGAGAA	CACTTTCCTG	60
TAAACGTGTT	TTCATGCTGG	AGCCAAGGTT	TTGACTTGGG	TTTGGATTTT	TATTTATTTA	120
TTTATTATTA	TTATTACCAG	GTTGCATCTA	AAGGATGTTT	TGGAGGAGCA	CAGAGTTTGT	180
CTGGTGAGGG	TAGGCTCTGG	GCAGATTTT	CTGTGAGTCT	CCCCTGCCTG	CGGCATCAGG	240
ATCATCCCTG	GTGCCCTGTG	GTGGCACCAG	GTGGCTGCCC	ACCCACAGGC	GTGGCCTTCA	300
CAGTGGGGGC	CATCTCAGCC	TGGGGTAGCG	ATCTGCCTCC	GACCTGCCTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCCTGCATC	GCAACAGCCA	GGAGGGCCAG	GCCACCCCAG	GCAGGAGGCA	GTGGGCTGGC	60
AGCCACCCCTG	GGCACAGAAG	AGCAGACGCA	GACAGTGCTG	GGCAACGAGG	GGCTTCTTTC	120
ATGGGCCCGC	CTGCCCTGTC	CCTCCCCCA	GGTCCCCACC	TTCTAGGGTT	AAAGTGCAGC	180
TGGGAGGGAG	GAGGCAGGCA	GAATTGGGGA	GCTAGAGAGA	GCCCAAGTGA	ACCCTGACTG	240
TCCACGCAAG	TCCCATGTCC	TCCTCGTCTC	GGAGTTCCTC	GAG		283

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC	TTCATGGCCT	AGACCTGCCT	CGAGTTCCTT	TTGTTATTTC	CCTGCATCTT	60
ACAACGTAA	GGCCTTGGTC	CCTGCTAATA	ATAAAATAAT	AATCAACTTT	ATAAAGAGCT	120
TACAATATGC	CAGATACTGT	ACTAAGTGCT	TTATATTTT	TTTTTGGGTG	GGGGGTGGCT	180
GTTGGGCAGT	GTCTCGCTCT	GTCACCCAGG	CTGGAGGGCA	GTGGCACAGT	CATGGCTCAC	240
TGCGGCCTTG	ACCTCCTGGG	CTCAGGCCTC	CCGCCTCAGC	CTCCCAGGTG	GCTGGGGCTA	300
CGGGCGTGCA	ACATTCTCGA	G				321

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC	TTCATGGCCT	ACGTAATTCT	GGAAAAGTGA	ATACTTGTGA	AGAGTCGTCT	60
TGAATGATTT	GTAAAAAATC	CTGTTCTTAT	ATTCAACGAG	TTTCGAATCT	TTGTCAGAGG	120
AGTATTACCA	TTAGATTGAA	AAAAAGGAAA	ATAAATAATA	AACACTTTTA	AAAAAAGTCC	180
CCATTCTCTT	ATTCTCACCT	TTAGGAAAAG	AGACTGACTA	ATATCTTCTG	CCACAAATAC	240
CGATGTTCTT	AAAAATATTT	ATGGGACTGC	TTTTGGCAAC	CAGCCCTATT	TTGTTTTCAT	300
ATCCCTTTT	GCTCCCATCT	TTCCAACTC	ATAAACTCGA	G		341

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCGGCC	TTCATGGCCT	ACTCGCCTCT	ACTAAAAATA	CAAAAATTAG	CCAGGCACGC	60
GCCAGGTGGT	GCGCACCTGT	AATCCAGCT	ACTAGGGAGA	CTGAGGCGGG	AGAATTGCTT	120
GAACCTGAGA	GGTAGAGGTT	GCACATAGCG	CCACTGCGCT	CCAGCCTGGG	CAACAAGAGT	180
GAGACTCTGT	CTCAAAAAAA	TATATAAATA	AATAAATGAA	AAAAAATAAT	TGTATAACAT	240
CTATACTATA	GCCTCGTAAG	CATTAGCTAC	TTAATATTTT	TGGTATATTT	AATAATTTTA	300
ATACAGCATT	TTTGATTACT	AGTGAACATG	AATATTTTCC	CATATTTGTT	AATTATACTT	360
TCCTCTTACA	GAAATCTGT	TTGTGTCCTT	CACCCTTCAC	TCGAG		405

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC TTCAGGGCTC CTCCTTCCTA GGCTAGTATT TATCCCACTA CATCTGACTC	60
ATTCTCTACT ATCGCTGTTG ATTTCTCTTT GGGTACTAAA TCTGTTGAAC ATGTTGCCAG	120
GCTTACTGCT GGTATTATGG GATAGCATTT GCCTGATGGC AGCTTCTAAA GGAGACTCCG	180
ATGGCACTAA GCAGTTTCCA AAAGTTTATC TTGCAAGTTC AACCCAATTC GAG	233

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCTAGA CCTGCCTCGA GATGTTTTTT TCGTTATTG AAATCTTGC TCITTTATTT	60
TTCAGCTCCC AGATCCTCTC CCTCTCTTTA GCTTTCCTG TGTTTGATAT CAAGAATATG	120
AAATGTGAAT TCCACGGACT CGAG	144

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GAATTCGGCC TTCATGGCCT AGGCAGGAAG GAGGCTGGAA TAAATAAAAA TAAAAATAGA	60
CAAGTAAGAC AGCATAAATA ATACATTTTT AAACATGTCA ACATTGATAA TACAATGAAG	120
ATTTACCATA AAAAGTATCA TATCTAACCA AGATATGCAA AAGATGCATT CAGTAAGCTG	180
TAACGTTGAG AAATGTAACT GTGAAATCAG CTCACCAATT CAAGTCACTA GGTTCGCCAC	240
TTGGACCGTC TTGGTTTCAG CGAGCATAGC GAGTGGCTGT AAGAAATTGT CCATGCCACC	300
AATTCCACTG CTACTTGCCC AGGTGGTCTC GAG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC TTCATGGCCT AGGAAGTGA GGAAGCTGG GTCGCTGCTG GAAGGGAGGG	60
AGGCTGACTC TCTACCCCTC ACCTCTGCAA GGAAGTGAAG CCTGTAGGGT TCGGGCTGTC	120
ACTGGCTACA GGCGGCATCT TTCTGTAAAA AGCTTTTCAG GCATGAAACC CATTTCGTGA	180
TGGACTGGGC TGTGTTGACG GTGGTGCTTG GGCCTTGCTG GCCAGGCCTC TCTGGGTCCC	240

CTCCCTGGCC TTGCTTCC TCTACCTTC TCGAG

275

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC TTCATGGCCT AGAGTCATAG GTCAGACCAC TTTCTAGGAG CTGTTCACTG	60
ATAAAATTAA TAACAGTGAC TTTTGAGTCA AAATAGATTT TTAAAGTACT TGATTTTCTC	120
TTTGATTGGG AAACATCTTT GTTTAGCTTA ATTGAAATGA TCTAAATAT TTGAAGGATT	180
TTATACTTTA CACAGAGGCA TGTATTGGA TAATTAGCTT TTATTAAACC CAGGCTTCCT	240
CGAG	244

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GCGATTGAAT TCTAGACCTG CCTGAACCCC ACCCTTCAG TCCTACTGG GCTGCCAAAG	60
TCATCTTCCC AAAACATGAC TTTTCCTCAG TCACCTTTCT TATTAGATTT TATCATATTC	120
CACATCCCCT CCCTGGCCCT CAAGGGTGCC TGTAACCTAG AACCATCTTA CCTTCCACC	180
CTTGTTTCCA AACCTTCGC TTTACTTAGA CATGCCTTCC CATTTCCTC CCGACCCACC	240
CCCCTCGAG	249

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC TTCATGGCCT AGAAAAAAC AAGTAGTTTG GCAAGGAGAG CAGAAAAATA	60
AAATTCCACT GTGTAGGCAT TTGGAGATTT AGCAAGAGCA ACCTAGAGTC TGCCCCCAGA	120
GACACTGCAC GTTGTTCCTG ACACAGAGGA TGCACTAATT CTATTTCTCTG TGCCACCTGA	180
AAAAATCATA ATTTGAGAAG AGAACTGTT AGGCCATTTT TAGTGAACATA TTTTCCAAA	240
CCCTCACGGA ACCCTGAACA GGGCGTGTCT CGAG	274

## (2) INFORMATION FOR SEQ ID NO:159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```
GAATTCGGCC TTCATGGCCT AAGCTTGCTC ACTCTTCTGT GTGTTTGAAA TAATGGTAAA    60
ATACAATAAT ATTGTCAAGC ACAGTGGATC GGAGATTTTT CTTCTCAGGA CTATTCTGCT    120
TATAGGTCTA CTTCTATAG CTATTGTCA TTGCCTCCT GGTCTTCTC TTTTCTTCTC    180
TCCTGTGCTA GATGCTCTCT CTTCTATCC CTCCTCTCT TCCCACCCCC ACCTCCCACT    240
TCTCTGTTTA TATCCTGATT TTGGTGGAAC ACATCCTCCA GGCTCCCTGG CACTCGAG    298
```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
ATGGCCTAAG GTGCCCNAGC TTGCCAATTA ATTCCCAGTA GAAATTTTAA AATGTTAAAG    60
ACAGTAATTA AAAAAAAAAA AAAACCAACAC TGTTTTGACA TTTTACCTCG TGCTTTGTGT    120
GTGACTAGAT TATGCACTAG AATTTTATTTC AGTATTCTTC CAAATAAGTT ATTTCCCAGG    180
TGTTGCTGG TATCTAACCA ANTANTCAAT AAAGTATTCT TGCTAAGTNG GCCATGAAG    239
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
GAATTCGGCC TTCATGGCCT AATATCATGA TCACTGAAAT TACATCTAGT GAAACACACA    60
CGTGCTTATC TGCACGTGTG TGTAAGTTAG AAAGAAAAAA CAAAGGCCTA ACAGTGATTG    120
TCTTAGGTTG ATAGGATAGT GGGTGGGATT TGCAGAATTT TTGTATCTGC AGAATTTTGT    180
CAAAGTGCCC ATTAGTTTTG TAAAGAAAAA AACCTAAATG TATAACTTCT AAAGAGATAA    240
TTTTTCTTT CATGTTTTTG CTACCTATAT CTAGGAAAAA AACTTAGAAT TGTAATTATT    300
TTGAAGCTCT GGAATTATTA TGTCAAAAA TTACAGAACC AAAAAGTCTC GAG          353
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GAATTCGGCC	TTCATGGCCT	ACTTGCTGTG	GCTGACTCGG	TTATTGACTT	TACTTCTTTT	60
CTTTTCAGGT	TTTTATGGGA	CTGTTTCTAG	CCCTGATTCA	GGTGTGTATG	AAATGAAGAT	120
TGGCTCCATC	ATCTTCCAGG	TGGCTTCTGG	AGATATCACG	AAAGAAGAGG	CAGATGTGAT	180
TGTAAATTCA	ACATCAAAC	CATTCAATCT	CAAAGCAGGG	GTCTCCAAAG	CAATTTTAGA	240
ATGTGCTGGA	CAAAATGTAG	AAAGGGAATG	TTCTCAGCAA	GCTCAGCAGC	GCAAAAATGA	300
TTATATAATC	ACCGGAGGTG	GATTTTTGAG	GTGCAAGAAT	ATCATTTCATG	TAATTGCTGG	360
AAATGATGTC	AAGAGTTCAG	TTTCTCTGT	TTTGACAGGAG	TGTGAAAAAA	AAAATTACTC	420
ATCCATTTGC	CTCCAGCCA	TTGGGACAGG	AAATGCCAAA	CAACTCGAG		469

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATTTATTCA	TTCTTGATTA	AATGCACTGA	AAAGTAAAGG	GTCTGTTTGT	GTCTGTTTCA	60
TGAAAATGCG	GTTAGAGAGG	TGCTATTCAA	GTGATTCTGA	AGGCACCCCA	AGGTATATCT	120
GTAATTTAAA	GATTACTGCA	AATATCTTTA	CTTTACTGTG	GGTTTTTAGT	ACATCTGTTA	180
ATTTAGTGTT	TCCTTGTTG	TTTGTAGAC	TAGTGTTCTT	CCATCCTTCA	ACTGAGCTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GAATTCGGCC	TTCATGGCCT	AGCATTTTTT	TTCTTTAAAT	TATTGTATCC	ACTAGTTCTT	60
CCCAGTATAA	AGGAATACAA	TGACTTTTGG	TGTGTTTCAT	ACGCTACAAC	CTTTCTAAAT	120
TCACATTATCA	GGTCCAGAAC	TCTTCTACTA	ACAATGCACT	TTTATAAAGC	CCTAACACCT	180
CTCCTGATCT	CTGTCTCACC	CTCCACCTA	TCTCACTGTG	GGATGGGAAG	GAAGTCAATG	240
GAAAACACAG	GAGCGCATT	TAATAATAGC	CCACATGGTA	TACTCGAG		288

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

GAATTCGGCC TTCATGGCCT AGCTCGATCC AAGAAGAAAA ATTAAATGA CAGCTTTTCC      60
CATTGATATA ATCATCTTAC TTGCTCTCT ACAAGAAATA TGCATTAGGA ACCTTCATTA      120
TAGGTCCACA GAAATAGCAG AACACAAAAG CGCCCCCTA CCCCCCGCC CCGGTAACCA      180
GAAATACACA GAGGCAGAG

```

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

GAATTCGGCC TCATGGCCTA GAATTAACCA ATTAAGAATT AATAAATTAC TTATAAAATT      60
AAAAATCAGG AATACCAGGC TTAATGCATT CATTATTCT ATTAGCAAA CTTTTTTTTT      120
TTTTTTGAAT GCCCAATG TCCTAGGTTC TGGAAATACA AAATTACTTG GTACCAGTAA      180
CTCGACTGTC ACCTTTCCAG CCATGGACTT GGTTCAGACA AACCCCCAGT CCACGGTTGT      240
CGTCCACTTG CAGTGCCCGC CGACTGTGGA TATATGCTGG GGATCCCAAC ACAACGCAGC      300
TACTCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

GAATTCGGCC TTCATGGCCT AGTAAATATT TTCTTCTACT TTGTGTTTTG CCTTTTGT      60
TTCTCAGCAT TATTTTTTGA AGACAAAAAG ATTGATTTTG AAGAACTCTA ATTTATCAGG      120
TTTTTTCTAG TAGTTTGTAG CGGATTTNTG CATGCTGCTT TAAAAAAAT CTTTGCTAAC      180
CCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```

GAATTCTAGA CCTGCCTCGA GCCTTGCCCA GAATCAGCAA GTAACTGCA CTAATTGTC      60
TTATATTTGA CTTTCTAACA CTGATTTTTC TGATTTTCC CTGTTGACC CTCCAATTGA      120
TAAAAATGTG TATAATTGTT CTGCTGCTTC TGCTTTGCC TGCTTTGGCT GCTGCATATA      180

```

CAGGTGAAGA TCTGGAAAGA AATGATGGAT CTACAGAAAA ACCCTACTTC GTAACCCCTA 240  
ACCTGCATGG AATTCTGATC AAGAAGCAAC TCGAG 275

## (2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GAATTCGGCC TTCATGGCCT AGTTTCACAT TGTCTGTACT GTGTTGTGCA GTACCAGAAG 60  
TTGCTGGTAG CTACTTGGTC TTCTGGGACC TGCCATTGCA GACGTGGTGA TTGTAATCTT 120  
AATCTTGTG AACAGGATG GATTATGAC TGGGATGGCC GGAAGCCACA CCAGACACCC 180  
AGTCACCTGG TCATGGGAGA GGTACTTTGT TGGCTTTTCA TAGTACTTAA CACTGTGAGC 240  
TGCTTCCTGA AGTGGCACTC TTAAGGCCAG GTGCCCCCAC CCTCGAG 287

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GAATTCGGCC TTCATGGCCT AAGACAGACA TTTTGGCAG AGCATAGATG AAAATGGCAA 60  
GTTCCCTGGC TTTCCTTCTG CTCACTTTC ATGTCTCCCT CCTCTGGTC CAGCTGCTCA 120  
CTCCTTGCTC AGCTCAGTTT TCTGTGCTTG GACCCTCTGG GCCCATCCTG GCCATGGTGG 180  
GTGAAGACGC TGATCTGCCC TGTCACCTGT TCCCGACCAT GAGTGCAGAG ACCATGGAGC 240  
TGAAGTGGGT AAGTCCAGC CTAAGGCAGG TGGTGAATGT GTATGCAGAT GGAAGGAAG 300  
TGGAAGACCT CGAG 314

## (2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAATTCGCCT TCATGGCCTA CACCAAGTTG AATCCCTATG CAGGAGGAGA CGGCCTTCAG 60  
AACAACTGT CCCCCAAGAC AAAGGGCACT CCTGTGCACC TGGGCACCAT CGTGGGCATC 120  
GTGCTGGCAG TCCTCCTCGT GCGGGCCATC ATCCTGGCTG GAATTTACAT CAATGGCCAC 180  
CCACATCCC TCGAG 195

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```
GAATTCGGCC TTCATGGCCT ACACTCCTGG TCATTTTGCA TTTTATCCAG CTTTTTTTCA    60
TCAACCATGT TATCCTGACA GACACATTTA TTGGATATTT AGTTGGAAAT ACCTTATGGT    120
TGGTTGCAGT TGGCTATTAT ATCTATGTAA CTTTCCTGGG ATACAGTGCA TTGCCATTTT    180
TGAAAAATAC AGTAATTCTT CTGTATCCAT TTGCACCTCT GATTCTGCTC AACTCGAG    238
```

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```
GAATTCGGCC TTCATGGCCT AGGCTAACGT AATTGAGAAA ACCAAATGAA ATATATCTTG    60
ACCAATAATT TAAAACCATA TCAGAGATTC AGTTTGTTTC TGTCTTCTGC TTTACTGATT    120
TTAGGATCAG CCTCATACAA AAGGGTAATG GTGGCAGCAG CTCCAGAACT CATATCATAT    180
CCTCCCATGT TAAAGTCAAA TGAGAAAAGT CTGTCTTCGC CCCAGGATCT CGAG    234
```

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```
GAATTCGGCC TTCATGGCCT ACTCAGTTCC ATTGTTAAGC AAGGAAAAAC AAACAATACA    60
TTGAATTTGA CAACCCACTG AAGTTGCAGA TAATGAGGAC TTACCATTGT ATACCATTAT    120
TCATCTGGAC CTATATGTTT CATAAGTTG ACACCATCCT ATTACAAGAA AAACCTAACA    180
GTTATTTATC AAGCAAAAAG ATAGTGGGTC TGACAAAAGA TGACGGTAAA ATGCTACGTC    240
ACACCCTCGA G    251
```

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GAATTCGGCC	TTCATGGCCT	AAACCACTGC	GCACCATATT	TCTTAAGGAT	GTTCTGAAGA	60
CCCATGAATG	TCTGGTCAAG	TCTGCTGATC	TCTTAATGAG	GGACAACCTG	TTTGAAATAA	120
TAACAAGCTC	CAGGACATTC	TACGTACAGG	CAGACAGTCC	AGAAGACATG	CACAGCTGGA	180
TTAAGGAGAT	TGGCGCAGCT	GTCCAGGCCC	TCAAGTGCCA	CTAGGCCATG	AAGGCCGAA	239

## (2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GAAAACCCCA	GATATTCCTT	ATTATGGAAG	AAGAAGCAGG	AAATATGTTT	TTGAATAATG	60
TGGGTCAGAG	AATTGTGCAT	TTATTATTGC	TAGGATGCAT	ATACACATTG	AACTCAGTCA	120
ACTTACTCTC	TCTAAATTAT	CTCACCGGTG	GAGACATTGC	CTCAGGAGTC	GAGCCCTGTG	180
GTGTGCCTCC	TGCTGTCAAC	ACATTTGACC	ACCTAACTGA	CCCCACTGTG	GTCACCTTTG	240
CCACCAATCT	CGAG					254

## (2) INFORMATION FOR SEQ ID NO:177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCGGCC	TTGCCAGTAT	TCATGCTGTT	GCTTCAGTCA	AGAATGAATT	CCTCAGCGCT	60
ACCTCTCTTG	ACCTTCACAT	CTTACTTAGT	GCAAATGCTG	TCTCCTCCTG	AGACTTGCCT	120
GACTTCGGAT	ACTCTCCCTG	TGACATCTTA	TCTAAAATGT	CAAGTGAGAC	TCGAG	175

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTCGGCC	TTCATGGCCT	AAGTGGCTGT	GTGGTATTTT	CTAAGTATTT	TTAAAATTTT	60
TCTCTCATTG	ATACCCTATA	AAAATGCAAC	TGTTAAAGAA	TTTGTCITTC	TTTCTCATT	120
TATTCTTTCC	AGAGTATATA	ACTAATTTAT	TCAGCATTCA	TTCATTGAGC	AGATATTTGT	180
TGAGCACTAA	CTATGTTTCAG	GCACTGGGCA	GGGATATCGG	GATACCAAGA	AAGCTCGAG	239

## (2) INFORMATION FOR SEQ ID NO:179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC TTCATGGCCT AGAAAATAAT TTAGAGAAAG AATAGAAAGT CATGGAAAAT	60
CTCATAGGTA GGAGACAGAA GAGAGAACAT TGTAATAAG TTTAAAAAAG ATAAGAAAAT	120
CAGGATAAAG TAGTATGGAC TCTGAGGTGG GAGAGAATTT TAAGATTAGC AGGAAAGTAG	180
TGTAGTTGGT ACTTTTGTAGT TATTAACAAA GCACTCACTT CTTACAGAGT CTCGAG	236

## (2) INFORMATION FOR SEQ ID NO:180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC TTCATGGCCT ACGAAGATTA TAATGTATTT TTATTCTGTT TTCAGCTTCA	60
TGTTTCCTGT TGCAGGTGGG ATAAGACCCC CTCAAGGCCT GATGCCGATG CAGCAACAAG	120
GATTTCTTAT GGTCTCTGTC ATGCAGCCTA ATATGCAAGG CATTATGGGA ATGAATTACA	180
GCTCTCAGAT GTCCCAAGGA CCTATTGCTA TGCAGGCAGG AATACCAATG GGACCAATGC	240
CAGCAGCGGG AATGCCTTAC CTAGGACAAG CACCCTTCCT GGGCATGCGT CCTCCAGGCC	300
CACAGTACAC TCCAGACATG CAGAAGCAGT TGGCCGAAGA GCAGCAGAAA CGATTTTGAAC	360
AGCAGCAAAA ACTCTTAGAA GAAGAAGAA AAAGACGCCA GTATCTCGAG	410

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC TTCATGGCCT ACACATTTGC ATTGTCTGCC CATGGACTGG TTGGAGCAGA	60
AACCTCCATA CCTCAGTCTC TTGGTATTTC TCTGCCCAAA CTGCTGCTTT TTGTTGGGAT	120
GTTTGTGTGT GCTGGGGTCT CGGCAGCATC GGCTGCTTCC CGGTGCGCAC TGACATGCAC	180
TTGTTCTCCA CGATGGCTTT CTCTACCTTC TGAGATGCTC CATTATCAGT CCTGCCTTTG	240
TTCCGGAGAG TTGAGATGGT ATCACTTCTC ATCCATCCTT AGAAATACCC CTCTCGAG	298

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCGGCC	TTCATGGCCT	AGGGGGCTGG	TAGTGAAATA	TTTGGTACTG	AAAGTGTGAA	60
GACCTCTGCT	GGGGACTGAA	CAGAGGGAGT	GTCTTCTGCT	GGTGGTGTGA	AATCTATCTC	120
ATCATCAAAA	TTATCTTCAA	ATTCTTAAA	GTCTATTTCT	GGGTCCTTAC	AGCAGGATAC	180
ACAGTTTGCA	ATTAACACTA	TTAATATTAT	TAAACTGCAC	ACACACAGGA	TCACAAAAGA	240
TGAGGAAACT	TCTGCAGCAG	GTGGCGCTCG	AG			272

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC	TTCATGGCCT	ACTACTTATC	ATCCCTGCTC	ACACACCCTT	GTCCAAGGCT	60
TTATGCATCG	GATTTATTTT	TCCAAATCAA	GAGGACAGTG	ATAGATGCAT	TTTCCCCCAGG	120
CTGTCTCAGA	AAGGTCGCTA	AATGTATACT	GTTGTCAGAA	TTGCTGAGAT	CTCCCCCAGC	180
TTTTGGTTTT	TGCAGCAGTA	AAAACCTTTT	CCACTGTGAC	TTATTTTCTC	TCTCAGGCAG	240
CAGACTCGAG						250

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC	TTCATGGCCT	AGATCTTCTC	CCCATTCAGC	AAAACCTTCC	CATTCCGGTT	60
AATGGTTTTG	ACAAGCAGGG	CACCACGGGG	CATAAAATTG	TATCATCCAG	CCTCCTTCCA	120
GCAGCTCTCT	CCAGTTCTTG	TCTGTGATGA	TGCGTACGTT	GCTCTGCCGC	CTGTGGGTCC	180
AGGGAGCACC	CCCAAGCAAC	AGTACCAGGA	CTGCCAGCGG	AACTGCAAGA	CTCCTGGAGG	240
GTGCCATGTC	TGCCACTTGC	CCACCTCACA	GCAAGCGTGG	CGGCCCAACA	CTAGGTTTTT	300
TAAAAACTGT	GACTATCAGT	GTTTTAAAAA	TTGCCCGGTA	ACTCTAGACT	TCAAAAGTGG	360
GATAAGTAAT	GATAAACCAC	TAATAAACCC	TGCTCGAG			399

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAATTCGGCC AAAGAGGCCT AAAAATTAAT ATTACCTTAT GACTGCCTTT ATCATGACTC	60
TCTTAGTGGG GATTTCTGTC CTCCACATGC CCTGGGGGAT GTGCAGCCCC CGTGCACTCC	120
CCGCCCTGGC CGGCCCTTC CCCCATGCC AGGTAGACTC TGAGCTCTTA GCCCAGCAAC	180
TCGAG	185

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC AAAGAGGCCT AGGGAATAA TCTTAAACAC TGAACCTCTT TTCAGCAAAT	60
TGGCTTTCTA GTTCTCAGC TCTCTCTTA CACCTCTAAA TCTCTTTCCT GGCAAGATCA	120
TTTATTTGCC TTGGTTTATG GTGATACTCT TCATTGTTAT ACTGGTGGGT GATTGTTTTA	180
ATTCATAGCT GTTTTTTCT ACTTCAGGAA GATGACACTG CTGGCTCTGC TGGCTCTGAT	240
GTTTACCTTG TGGCTAATGC CTGTGTTTGC CTGTGTTTAC ATTTATTCCA CGATTCATTT	300
GTTAACATTT ACTAAGCTCG AG	322

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCC AAAGAGGCCT ACTCATAACA GCGTCAGAGA GAAAGAACTG ACTGAAACGT	60
TTGAGATGAA GAAAGTTCTC CTCCTGATCA CAGCCATCTT GGCAGTGGCT GTTGGTTTCC	120
CAGTCTCTCA AGACCAGGAA CGAGAAAAAA GAAGTATCAG TGACAGCGAT GAATTAGCTT	180
CAGGGTTTTT TGTGTTCCCT TACCCATATC CATTTGCCCC ACTTCCACCA ATTCCATTTC	240
CAAGATTTCC ATGGTTTAGA CGTAATTTTC CTATTCCAAT ACCTGAATCT GCCCCTACAA	300
CTCCCCACCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

GAATTCGGCC AAAGAGGCCT ATTATGCTGG TGCTGTCTAC TAATTTCAAG AAAAAGTACA      60
AGTCTGGCTA GACTCTGCTA CCGCCTAGCA CTGAGGTGTG GTCCTTTATC TGTATTACA      120
TTCTTCGTGA TAATGAAATT CTGAAACACA TGCTCCAGGC ACCTTTGTAA ATGTGAAGGT      180
GAATAAAGTA TTTGTTGTT GTCTGAAAAG AGATCTTTGA AATGTTAAGT TGCCACAGAC      240
CCAGACCAAG GAGCCTGCTG AGAGTTTTAA AGGCTCTTAT TGGATGACAG TAGATTCTTT      300
CCTTGAAATG TCTATAATGA ATATTCAAGA ATGCTCATTG TGCATGAAAT TTGCAATTTT      360
AATTATCAGT GAAAGAAAAG ATTACACAGT GCTAAATGAT TGCCATGGAA AAGTTATGGC      420
TACCTCTTGG AGTAGAGAAA ATCTCAAAGG CCGCTACTCG AG                                462

```

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```

GAATTCGGCC AAAGAGGCCT AGTGGGCAAC TTGGAGAAGA GTGAAAAACA CTAAAGAATC      60
ATCTCTTTTC CGAGTCACAA AGTCCCATGA ACTTTGTGAC TCAGAGACAC TTTTCGTGAA      120
AATTACCTTT CGGCGGGACA CCGTCTCAGG GCAGCTTTT CAAGGCTTCG CTTGACATGA      180
TTTCTTCCCT TTCATCAGTC ACTTTGGATC CAGCTGAATA TCTCTCTCGG GTGAGAGCGG      240
ATGTGGACTG GCCTCCACA GAAGAAGAGT AGGTGGCTTT GGTGGGGTT GGGGTGCGG      300
CTGGCTTCTT GGTCTCGAG                                319

```

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

GAATTCGGCC AAAGAGGCCT AGTGAAGAAG AAGAGACTGT NAAATAATTC TGCATATCCT      60
CAGTGGATAA TTCTGTNACC TATCTGTCAG CTATTCCATA TCAATAAAGG ACACAGCTGG      120
TAATCCAAAA GGAAAGGATC TCTTGATGAA AGTGTTCTGC CATTCTTATT AAAGTCAACA      180
TACAAGATAC ACTCTTAGTG ATTTTGAAC CCATAATTAT ATTTGCTGA TAATAATTGG      240
CACTTAACGG TTACAGAACA CTTTCACTGA TATTTTCCTT AGTGAATCTT AACAACAATT      300
CTACCAGTAA TTTCTAATAT TTGCCATGAT TAGACTTTCA AAATTAGTCC ACGCACTCGA      360
G

```

## (2) INFORMATION FOR SEQ ID NO:191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTCGGCC	AAAGAGGCCT	AAGAAACATG	GCGGCCGCGA	CGTTGACTTC	GAAATTGTAC	60
TCCCTGCTGT	TCCGCAGGAC	CTCCACCTTC	GCCCTCACCA	TCATCGTGGG	CGTCATGTTT	120
TTCGAGCGCG	CCTTCGATCA	AGGCGCGGAC	GCTATCTACG	ACCACATCAA	CGAGGGGAAG	180
CTGTGGAAC	ACATCAAGCA	CAAGTATGAG	AACAAGTAGT	TCCTTGGAGG	CCCCATCCA	240
GGCCAGAAGG	ACCAGGTCCA	CCCAGCAGCT	GTTTGCCGAG	AGCTGGAGCC	TCAGCTTGAA	300
GATGATGCTC	AAGGTACTCT	TCATGGACCA	CCATTGCTG	TTGGCAAGAA	ACGGCTTTAC	360
TTACAAAACA	GTCTCGAG					378

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCGGCC	AAAGAGGCCT	ACTCTGAATT	AATGCAAATT	CCCGTTGTAC	TGTATTTAAT	60
TATGCACAAA	ATGGTGCCCT	TGACTCAGAT	TTCACTGAAG	AACTTCATT	TTTACTTTT	120
AAGTCTCCAA	GTAGGAAATT	CAATTAGCGT	TATGAAAGAA	ACACTAAAAC	TCGAG	175

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GAATTCGGCC	AAAGAGGCCT	AGGCAGCAAT	GTTATCTGTC	CTTCATTCTT	GCATGTTTTT	60
GGAAATTGCT	TTTGCTTTTA	CTTTTGGTCG	TCATGGCAAT	CACGTGCCTT	CTCTGGTTCA	120
TTTTGCACAG	ACCTGCCTAG	AGCTGGAACG	TTACCTCCAG	AGCGAGCCCT	GCTATGTTTC	180
AGCCTCAGAA	ATCAAATTTG	ACAGCCAGGA	AGATCTGTGG	ACCAAAATCA	TTCTGGCTCG	240
GGAGAAAAAG	GAGGAATCCG	AACTGAAGAT	ATCTTCCAGT	CCTCCAGAGG	ACACTCTCAT	300
CAGCCCGAGC	TTTTGTTACA	ACTTAGAGAC	CAACAGCCTG	AACTCAGATG	TCAGCAGCGA	360
ATCCTCTGAC	AGCTCCGAGG	AACTTTCTCC	CACGGCCAAG	TTTACCTCCG	ACCCCATTTG	420
CGAAGTTTTG	GTCAGCTCGG	GAAAATTGAG	CTCCTCTGTC	ACCTCCACGC	CTCCATCTTC	480
TCCGGAAGTG	AGCAGGGAAC	CTTCTCAACT	GTGGGGTTGC	GTGCCCGGGG	AGCTGCCCTC	540
GCCAGGGAAG	GTGCGCAGCG	GGACTTCGGG	GAAGCCAGGT	GACAAGGGAA	ATGGCGATGC	600
CTCCCCGAC	GGCAGGAGGA	GGGTGCACCG	GTGCCACTTT	AACGGCTGCA	GGAAAGTTTA	660
CACCAAAAGC	TCCCACTTGA	AAGCACACCA	ACGGCTCGAG			700

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

GAATTCGGCC AAAGAGGCCT AGAAAAATAC TTGGGCAGAA AGAAAAATATC ATCAAATAAC      60
ACCTATTTCT TTTCAGCTAT AGAGATGGCT GGATATCAAA AGCACCACGG GAGCTTTGCA      120
ATTGTCTGCC TCTTTTCAGC CCTCAGCTTG ACTCTCAGTT TTCAAGAGGG AGAAAAATGAA      180
TGTTTCCCAG CATTCTCTGT CCTTTGCTCC AAAGAAGAGA GCAGGTGTTG GCTTCCAAAC      240
CTTCCGTATT TTCTTATGTC TGTTAGGGGG ATCAACTGCA TGTTTCCTGA GGGAAAAGGG      300
TGGCTCACTG ACCTACTTGA AGGCATTCTC TCAGTGGGAG CTGGGCAAGA GAATCCAGGG      360
ATTTCTTTTG CAGGTTTCTG CGCAGTGCCC CTGCCATCAA GCTGCCTAAA ATGTGAATAT      420
TGCTTCCCTG CGTTTCAGAG GTGGCCGCTC GAG                                     453

```

## (2) INFORMATION FOR SEQ ID NO:195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

GAATTCGGCC AAAGAGGCCT ACAAATGTG AATGGAACAA ACCTGCACGT GTACCCTTGG      60
ATGTGTGGAT GTTCTTTGTT TTTATTTGTT AAACCTGATG TCTTGTCTGT ATGACACATT      120
TATTGGAAC GTTTTTTCCC TATTCTGTGT CTTGTATTTT ATTTTCTCGT GTTCTCCAAA      180
GAGCAGATAT TTTAAATTTT TATATAAATC CAGTTTGTCA ACATTTTAA AGGGTTCATG      240
CTTTTGTAT CCTATTTTCTG AAAACTTTGG CTACTTCAAG GTCACAAAGA TTTTGGATT      300
GTTTTAATCT ACAAGTTTTA TAGCTTTGAC TTTATATAT AAGTCTGATT CATTTGGAGT      360
TAATTTTGT GTACAGTGTG AATTAAGGGT CTAGGTTTCTT TTATTTTCTT ATGAATATCC      420
AATGGTTCCT CGAG                                     434

```

## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

GAATTCGGCC AAAGAGGCCT ACAAACACAG AACATTTCCTA TCGTTGCAGA GAGTACTATT      60
AGAGAGCAGT ATTCCAGAGC CTGTGATCTT AATCACTACA CCTAAAGCCT CCCAGTTGAC      120
AAAGTTACCA CCTTTTTTTG GTGTGTGTGC ACGTGCGTGT GTGTGTGTGT AAGTATATAT      180
AATTTAAATC ATTCCATTAA ATTTACCTCT GAAATTCAAA AGACTGAAAC AGATCTTCTT      240
TTTATCAAAT AAGTTGATTG CAGAGATTAT ATTGGTGTGTT ACATTTTCAGG CAACCTGCTC      300
ATGAAATTAT CCATTGCTCT CGAG                                     324

```

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC AAAGAGGCCT ACTCCTCCGC CTGCAACCAT TGTTTCCTAC CACTGGATTA	60
TTCTGAAGCA AATTTTAGAC ATCATATATA TTTATCTCTG AAAGAGGACT CTTAAAAACA	120
TGCACCTTATA CCTCTATTAC ACTGACAAAA TTGGTAACAA TTCCTTTATA TTATCAAATT	180
TCCTTATTGA GTTCCTGATG TTCAAATTC TGATTCTCCA GATGCTCCAA ACTTCCAGAA	240
ACACAGATTC CCAGATGGAA TCCTGGGGAA GGCTCGAG	278

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTCGGCC AAAGAGGCCT ATTTTCTAAT AAAAATCTATT TTATGGTAGG TTTTGTGGAT	60
TATTGAATAC AATCTGGCAT TCTGTTTAAT ATGTATGTTT TCCTGAATGA GGGGGTACAT	120
TGTAATTTTA ATTATTAAAC TCACAATGTT TTTGGTTTAA AAAATAAAAA TTTTAGGAGC	180
AAGCAGTGTT CTGCTTCTCT TTTCTGAAGA TGATTCTCAA TCGAATGACT CAAGTGATTC	240
TGATAGCAGT AGTAGTCAGA GTGACGACAT AGAACAGGAG ACCTTTATGC TTGATGAGCC	300
ATTAGAAAGA ACCACAAATA GCTCCCATGC CAATGGTGCT GCCCAAGCTC CCCGTTCAAT	360
GCAGTGGGCT GTCCGCAACA CCCAGCATCA GCGAGCAGCC AGTACAGCCC CTTCCAGTAC	420
ATCTACACCA GCAGCACTCC ACCTCGAG	448

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGGCC AAAGAGGCCT AACTTTTGTA ATTTGAATTG GGTCCCGCTT AGTTCCTTGAA	60
TTGTTATGAA AATCCTATAT CTGTTTGAT ATTTGCAAAC CCTTGATATT ATAATTGTTG	120
ATATTTTCCC TTTTAAAAA ATACCATTGA AATCAGCATG AAAAAATAA CACTGTGGGC	180
ACTCGAG	187

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:



```

GAATTCGGCC AAAGAGGCCT AGACCAGAAT AAGCCTTTTA AGGTAAACCT CAAAATTATC      60
ATTTTATGGT AATACTGACC ATTTTAGTCC CTTAGGTTTG ACATGGGAGA TAGTGACTAC      120
ACTGGTGTCT GACTTTTTTC CTAGAGATT CTCCCTGAAA AATACAAGGG CTGTTGGTGA      180
GAGCAGACTT GAGGTGATGA TAGTTGGCCT CTGGTCTACA AAGATTTTCAT AACTCCTTGG      240
AAAGCTTCTT ATAATCATTC TTAACCTTCT GGTAGCTAGA AATTTAGAGT AGTTGAAATC      300
TTTAGGAATG AACTTCTGAG GGCCAAAAAA TGTGACTGAC AACTCGAG      349

```

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```

GAATTCGGCC TTCATGGCCT ACATCACCAA TTCGGCTGGG TAAGGGTCCC CATGAAGGCG      60
CAGCCGGGTA TAGAGGTGCA GGGGAGAGCA GCCTGGGGAG TCCCTATCTG GATAGGCTCC      120
AGCCTGGGTC GGGGCGGTCC TGGTGCCCGG TGAAGCGTCA AAAGAGGGAG CCTGAGCGGG      180
GCAACGCAGA AGGGTGGAGA GGAGGGGGTG GCGAGGGCGG GCAGCGAGGC CTGGAGCCGC      240
CAGGAGAGGG GCGGGGGGCG GCCCTTCTCC AGGAATTTCC GGGGATCGTG TTACAGCGTT      300
GGCGGAGCCC GAGCGGAGTG GGAATCGAG      329

```

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

GAATTCGGCC TTCATGGCCT AGAAAGGGGA GGGAACTGTA CAGGCAGGTG TGGGATAGGG      60
ACTTCTCTTC CGGTCAGAGC AAGGGTCGTC CGAAACCAAA ACAACCCTCT TCCCTTCATC      120
TCGCCCCGGA TCCAAAGTCT TGGGGCTAGG CTGGGGCGGG AGTGGCACGG AGATGTAGGA      180
ACACTGCCTT TCGTTACTTC TCCTGCCATG GCTGACCTTT TTGTCTCTTG TTTCATGGTT      240
TTACACGTAT GAATGGCTTG AGACTGAGGA TTTAGGGAAG AAGCGAAGGC ATCATCTAGG      300
GCTGTGCTGT GCCAAGTTGA GCAGTTGTTT AAATGTTAG AATTTTGTAC TGGTGTAATA      360
ACCCTCTATG CTCGAG      376

```

## (2) INFORMATION FOR SEQ ID NO:203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

GAATTCGGCC TTCAAGGCCT ACGTGAAACC CCATCGGCTT CATGGCTCC TTGATTAAAA      60

```

CCACGCCCGG CTNTCTGCCC TCTTTGATGC TGCTGGGCCA GGTGCCCCAG CCATATCCCA	120
GCCCCGTCTG CAGGGAGCCG GAGGCGCTG CTGCTGCTAT TGTGTGGATG CCGCGCGTGT	180
CTTCTCTTCT TTCCAGAGAT GGCTAACAGG GGCCCGAGCT ATGGCTTAAG CCGAGAGGTG	240
CAGGAGAAGA TCGAGCAGAA GATCTCGAG	269

## (2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTCGGCC TTCATGGCCT AGATGTGTTG AACCTTATTC TTGTACATTC ATTCAATCAA	60
GGCAAACCTTT TATAATTTTT CTTTGTGTTT CAATGACCTT GAAATGTTAT AGCATGGTAA	120
TATTCTATGC AACTATAGTT ATACTTTTTG GTTTGACACT GTATTTTTTC ACATTGATTT	180
ACTGGTTGAG GCTCGAG	197

## (2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTCGGCC TTCATGGCCT AGCAAGACCT TTAAAGTATA TACTCTGAAA GTGTGGCTAA	60
TATGATCATG ATGCTGTAGG AAAAAAGGT TATATGTCCA AGTGTATGTA CTTGTAAATG	120
TGCCTAAAGA AACCTGGAAG GATACACAGG TCTTCCTGG GGTACAAGAC GGAGAACTGG	180
GATCATCATC TTAACCTCTAC TCTTCCTTTT TACTCTTCTG TCCTCTTAGA GACTTTTGCC	240
TGTATACATG GATTACTGTT ACTTAGCAGG GGCGACCGGT TGGCCAAAGC CTTGGTGTGC	300
CCTTGGCACA ATTCTGCCAA GACCCTTACC CTCTCCTCTC CTCANGGCTC CCTTAACCCC	360
TCTCCCCACA TCTGGAAAC CCTGGATACA TTTTCT	396

## (2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTCGGCC TTCATGGCCT AGGAAGAGGT TGAGAAGACT CCTGGGCTTC AGCCTCTCCC	60
ACCCAGCCCT GCCCTCACC TGCCTGCCCT CCCTCCCC ACTCTATACT AGGGACTGGA	120
TCTCAGCCTC TGATCAGTTT CACAAAGTTT GTTCCCTAAG GAAATCAAAT CCCATTGTCA	180
CCTAACTCTG AAGATCTAAA TAGCCCTTGG ATCAGTACGG GAACCCCAA TCCACAGGG	240
CCAGATGTGG AGTCTGTGTC TGCCCCCGTC TTCTCTCCAT CCTCAAAGCC CCCACTTCTC	300

TCCAGGCTGC TTCTCGAG

318

## (2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GAATTCTAGA TCCTGCCCTC GGAACAATGG GACTCGGCGC GCGAGGTGCT TGGGCCGCGC	60
TGCTCCTGGG GACGCTGCAG GTGCTAGCGC TGCTGGGGGC CGCCCATGAA AGCGCAGCCA	120
TGGCGGCATC TGCAAACATA GAGAATTCTG GGCTTCCACA CAACTCCAGT GCTAACTCAA	180
CAGAGACTCT CCAACATGTG CCTTCTGACC ATACAAATGA AACTTCCAAC AGTACTGTGA	240
AACCACCAAC TTCAGTTGCC TCAGACTCCA GTAATACAAC GGTCAACCACC CTCGAG	296

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GAATTCGGCC TTCATGGCCT AGTCTCTTGA AAAGCCGCAT TTCCAGGCGC TTGGCCAGTG	60
GCCTGGGAAG TAGCCTGTGC TTGTATTGAG ACAGTCCCCC AGCAGCAAAC CATGTTCCAG	120
TCATTCCCTT TCCTACTTTG GGGATTGTTG CCTTTTCTGC TTGTTTAAAG TAAAACAAGC	180
ATGTACTTGT TTGTATGTAT GTATGTATGT AGTTGTACGG TGGGCACAAA TAAAAAGAGG	240
GCTGTATCCA AATAAATCAT TTCTGGCTGC TCACTGGCAC AGTCCCTTTG CTCCTCCCC	300
TCCTGGCTCG AG	312

## (2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATTCGGCC TTCATGGCCT AGGCAGCGTT TCACCGCTGT GGAGGACCAG TATTACTGCG	60
TGGATTGCTA CAAGAACTTT GTGGCCAAGA AGTGTGCTGG ATGCAAGAAC CCCATCACTG	120
GGAAAAGGAC TGTGTCAAGA GTGAGCCACC CAGTCTCTAA AGCTAGGAAG CCCCCAGTGT	180
GCCACGGGAA ACGCTTGCCCT CTCACCCTGT TTCCAGCGC CAACCTCCGG GGCAGGCATC	240
CGGGTGGAGA GAGGACTTGT CCCTCGTGGG TGGTGGTTCT TTATAGAAAA AATCGAAGCT	300
TAGCAGCTCC TCGAG	315

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

GAATTCGGCC AAAGAGGCCT AGGAAGATGG CGAAGGTCTC AGAGCTTTAC GATGTCACTT      60
GGGAAGAAAT GAGAGATAAA ATGAGAAAAT GGAGAGAAGA AAACCTCAAGA AATAGTGAGC      120
AAATTGTGGA AGTTGGAGAA GAATTAATTA ATGAATATGC TTCTAAGCTG GGAGATGATA      180
TTTGGATCAT ATATGAACAG GTGATGATTG CAGCACTAGA CTATGGTCGG GATGACTTGG      240
CATTGTTTTG TCTTCAAGAG CTGAGAAGAC AGTTCCTTGG CAGTCACAGA GTCAAGCGAT      300
TAACAGGCAT GAGATTGAA GCCATGGAAA GATATGATGA TGCTATACAG CTATATGATA      360
GGATTTTACA AGAAGATCCA ACTAACACTG CTGCAAGAAA GCGTAAGATT GCCATTCGAA      420
AAGCCCAGGG GAAAAATGTG GAGGCCATTG GGGAGCTGAA TGAGTATCTG GAACAATTTG      480
TTGGAGACCA AGAAGCCTGG CATGAACTTG CACTCGAG      518

```

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

GAATTCGGCC AAAGAGGCCT AATTGAATTT CATTTCTTT GTAGACTAAT GTTACAATAA      60
ATAAATGGGA ATTTTAAATA CCTGCATGTT CTGTTTTTCT CTTTTTCTT TTTTCAGCCA      120
TAATGAAAGG AAAGTGACCT GCAAACATCC AGTCACAGGA CAACCATCAC AGGACAATTG      180
TATTTTTGTA GTGAATGAAC AGACTGTTGC AACCATGACA TCTGAAGAAA AGAAGGAACG      240
GCCAATAAGT ATGATAAATG AAGCTTCTAA CTATAACGTG ACTTCAGATT ATGCAGTGCA      300
TCCAATGAGC CCTGTAGGCA GAACTTCACG AGCTTCAAAA AAAGTTCATA ATTTTGGAAA      360
GAGGTCAAAT TCAATTAAAA GGAATCCTAA TGCACCGGGC GATCTCGAG      409

```

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

GAATTCGGCC AAAGAGGCCT AGTACAGTCC CAATCAAGAA GCCTTATTAA CCTTCTGTGT      60
GAGGGACTAG ACTCAGTGTT GGGTTTGGAG GATCCACTGG TGAGGAGCAT TCAGTCTAGC      120
AGGAGAAATG TCAGCATTAT TTATTACACA ACAAGATCTG ATGCATTGAG ATGTACTTAC      180
AGGTCTAGGA ACTGTTTCTG GGAGCACAAG TGAATGAGAG AGAGAGGGAG AGAGGGAGAT      240
TGAGTGAGTT AGAGAGTTGT TGGTCTCTCA CAAGGAGCAG TAAAGTATTT TAAAAATAAA      300
AAATAATAAG GCTGACTCTG TGTCTGCTCT AGGGGTTGGC CATGCTCCAC AAAAAGCAGT      360
AAAGTGTTTT TTGTTTTGTT TCGTTTTTTT TTTAAAGACA GACGTCTCGA G      411

```

## (2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
GAATTCNGCC AAAGAGGCCT AGTTTATCT TCTTACCTAT TTACTGAATG CNACATTACT      60
GCACACCAAG ACAAAGAGC TCTCCAGGAA AACATTGGAT ATATTGAGAG CATTAAAAGA      120
TACTGCAAAA GCTCTAATAA ATTCAGTCTG CTTATTTTCC AAATTCATA AACTACATAC      180
TTAGGAAACT GTGCTTTCAG TGAGCTAAAC TTCTTTTTTT AAGTAACTAT CATAGTTTAA      240
AGAAAAACAT TTAAAGAAGA CAAAAGTAT TTATTAAGCC CATCTAAAAG GCTAATGCAA      300
ATTCCCAAAA AAGGAGCACA TAGAGATAGG CATCTCGAG                               339
```

## (2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCCT CGAGACACTA GCCCTTTTTT      60
CTGTTGGTTT AGCACAATA CTCCCTCCT CCGGCACCTC CAAACCTACC CCACAGTCAG      120
TGTAATTGTT TTATATATAT TTAATCTTAT TCAATGGAAA CCATGCTTTT GTCGTTTTAT      180
ACTTTGCTAG GTAGACTTCT CGAG                               204
```

## (2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
CTCGAGAGGC GCATCTTCAC TGGCATATGA CAGGCTGTCA CTGCAGCTAA TGTTGGTACA      60
GTTTTTCCAA AGACCTACTG ATGCATCTAC CGTATTGGAA ACCAACCAGA CATTGGCAAT      120
GGTGCTAACA AATAGCATAA TAACAGTAGC GATGTGGACC ACAAAGATAC CAGCCAGCAA      180
TACCAACATG TTGGCTCTTT TTTTTTGGT AACTTGTGAG CAAAGAGAGT TCTGAAGGGT      240
CCCAGCGACA GAGGCACTCG AGGCAGGTCT AGAATTCAAT TAGGCCTCTT TGGCCGAATT      300
C                                                                                   301
```

## (2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC	AAAGAGGCCT	AAAATATTTG	AGTCTAACT	TATAAATTTT	GCATTCTCCC	60
TAACGAAAAA	ATTTCTATTA	CTGTGGTGGG	TTTCTTTAAA	TTTTGAATAT	AGTTACTGAA	120
ATATTAATTC	TTTCAATTAA	ATTTATATTT	ACTCACTGGT	TCCTTCCCCT	TCTTTAAGGA	180
GACAGAAAAC	ATTAACACTT	TTTAACCTCT	CATTGTGTTA	AAAATTTATT	GACCTCTCCT	240
CTGAGACAGT	TTGTATTCCT	AGATCTCTTT	AAACATAAAT	ATGCTTATTT	TCAAGTTTTT	300
GTCACAGTAT	TCACTCGAG					319

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC	AAGAGGCCT	ATTTAGATTT	AACCCAGTTT	GTAGACATTT	GCATAGATCA	60
AGCAAACTA	GAAGAGTTTG	AAGAGAAAGC	ATCAGAACTT	TACAAGAAAT	TTGAAAAGA	120
GTTTACCGAC	CACCAAGAAA	CTCAGGCTGA	ATTGCAGAAA	AAAGAGGCAA	AGATTAATGA	180
GCTTCAAGCA	GAGCTACAAG	CTTTAAGTC	TCAGTTGGT	GCCTTGCCAG	CTGATTGTAA	240
TATTCCTTTG	CCTCCCTCTA	AAGAAGGTGG	AACCTCGAG			278

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC	AAAGAGGCCT	ACCTGGCTCA	TTTATAACCT	CCTCGATCCT	ATTACTGATT	60
TGCATTCTTA	ACTACAGGTA	AGAGAAAACC	AGTGCAACCT	AGCTTTCAAT	AGACAGGAAT	120
TTGCTGGCTC	ATATAATGA	GACATCCAAT	AAAGAAGAAA	AGTTGGAAAA	AATGTGTCAA	180
ATGTAGCATC	CTCTCTCTCT	CTTCTCTCT	CTCTCTGTTT	TTTCACCTAG	GCTTGTGCCA	240
TAAACCTGCT	TCTACATCAG	TTACTGTGGT	TATGGGCGTC	TTGTTGGCTG	AGCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```

GAATTCGGCC AAAGAGGCCT ACTTAGCAGA ATATATTCTT TAATAGCTCC CATAAAGCAA    60
ACAAACCCAA AATATATTCT CCTGACCCTA CATTCACCTC CAACTATCAC CCTACATCTA    120
CATTCTCCTT TTCATACCAA ACTTTTCCA AGCAGTTGTC TATATTTATG TCTCCACTTC    180
TTTACCTCCT ATTCTTGCTT CAGTATGCTT CAGTTGAGCT TCGTCCCCCT GTAGTCCACC    240
ACCAACTCGA G                                     251

```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

GAATTCGGCC AAAGAGGCCT AGATTGATTC TGTGTTGTGG TATTGGCCCT TACATACAAC    60
TGGAGGAAGT GTGAATTTC AATGTTGAT AAATTGGACT GTCATGATTC TTTATAATTA    120
CTTCAATGCC ATGTTTGTG GTCGGGCTT TGTCCCTCTG GGGTGGAAAC CGATGTGTGA    180
TGAAGATGGA CCATCACTGT CCTTGATCA ACAACTGTTG TGGTTACCAA AATCATGCTT    240
CGTTCACACT GTTCTCCTT TTAGCACCAC TGGGTTGTAT CCATGCTGCT TTCATTTTGT    300
TGATGACTAT GTACACACAG CTTTATCATC GGCTCTCCTT TGGGTGGAAC ACAGTGAAGA    360
TCGACATGAG TGCAGCAGCC TCGAG                                     385

```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

GAATTCGGCC AAAGAGGCNT ACCCNGATTA TAGTTTTTGT ATTGTTTTTA CAATTTTTGT    60
GAATTAGGAT CCAAATAAGG TCTGTAAATA TTACATTGGG TTTAGGTAAT CGATACTTTT    120
TTTCTTTTAA TCTATAAGTT TTCCTCTATC TTTTATTGT GGTATTCCC ATACAATTGG    180
TTTGTTGAAG AAGCCAGGTC TTTGCCCTAT AATACTTCTC AGAATCTAGA TTGTGTTGAT    240
GAGATCCCAG TGGTTTCATG TAATATGTTT TTTGTCCCT TGTATTTTCT GTAAATTTTG    300
TTTATTTTAT TTTTATTATT TCTATTATTT GAGATGGAGT CTTGCACTGT CAGCCAGGCT    360
AGAGTACAGT GGCATGATCT CAACTACCG CAACCTCGAG                                     400

```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

GAATTCGGCC AAAGAGGCCT AAGAGCCTAT AAGGTTTACA TATTTCACTG GAGAGAGAAA      60
TAGGGACATA CAATAAATGA TTTTATAATA AATTTCCATG AAAAGTGAAT CTGAAAACCC      120
CACCGGAAGG CAGAGTAGTG CAGCCAAAGG AGCATGAATT GTGGAATCAT ACAGCTCTAG      180
GTTTCAGATCC TACCTTTACC ACTTGATAGC TAGGCAGACT TCAACAAGTT AGTCTAATTT      240
GAGCTTCAGT TCTCTCATCT GTGAAAAGA GAAAATACAG CCACTTTATA ACATTATTTT      300
AGATGCCATA AGGTAGGTAA AGTGCCAGAC ACATAGATTC AAAAATCTCA ATAAAAATAGG      360
AAGGCTGGAA TTTCCAAAT TTTTCTTGC TTTCACAATC TGGGTTCTAA ATTTATTATT      420
ACTCTACCCA TCACTTCCTC CTTCTCCCTC CACAACCTCA CTATAAGCCC AACATCTCGA      480
G

```

## (2) INFORMATION FOR SEQ ID NO:223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

GAATTCGGCC AAAGAGGCCT AGTGTCATGT AGAGGTCTCA GCATTTCTCT TAGTATTGAA      60
CTGTATTAGT TTTACATAAT TCCTCTTTTG TTTAGAGTAT AACCGCTTCT TACATTTCCCT      120
TCAGTCGTTT TCTAAGAAG AAATTAATCT TTTTAGAAAT CCTGGCAGTT ACCCGCAAT      180
TGATGTTTTG GTGGAAAATT AGAGCACACC AGTTTGTCAT AACTTTAAGA AACATTTTCA      240
CTTTATTGAT ATTCTGAGGA TTTTAGTGAT TTGGGTAATT TGGGTCTAAT AAAGAGTAAA      300
TTGTTGAATA CTCATTTGTT TTGAGTCATC TATATTTTTA AACCTTTCT TTAGTTGTTT      360
TTTCATCCCT AATACAAATG CAACTTTCCC ACTTGCTCGA G

```

## (2) INFORMATION FOR SEQ ID NO:224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

GAATTCGGCC AAAGAGGCCT AAAGTGATGT CTTCATTG CTGGATAGGA CATGCTGACT      60
GATGACCTCA CAGACTGTTT TTATGCCCTC ACTACTCACC TCACCACCTA CAGTCATAGG      120
CTGACTAGGA GTTGGTTGTG TACATTCCTA AACCTTTTGG CCCTCTTTAT TTGCTTTTCT      180
AAGTGTGTAT TCAGTACTAT GTAAATTGAT AAAACATGAG TGTGAAAATA TTTTTTTTTG      240
CTATAAAAT GTAAATTGAA TTCTTTGGGG AAGAGCTGAT AAAATATGTC ACTTAAAGAT      300
CTTGTTAAAT TAGATGAGGG AGATATAGAT GACAGAAACT CTTTCAACAA ATATCTAAAA      360
AGATGTGCCA CTCCAATTAT TTTGTGAGTG TCTTCAAGTT TTTGTCCCAC TTTAAAGAAA      420
ACCAAACCTGG CCATCATAGC CAATGAATTA TGCAGGAGTC TCGAG

```

## (2) INFORMATION FOR SEQ ID NO:225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

GAATTCGGCC AAAGAGGCCT ACACATTATA TTAGATTTC TAGAACTGT TGGAAATATC      60
TAGCACATGT GCTTTATCCC ACAATAATTA CATAGAAAAT TAAAAAGAAT TAATTCTAAT      120
GTAACCATCT TTTTACTTGA CTTTTTTTTT TTTTGCTCTG CTCACAGGTC TAATGTGTGT      180
TATTCTCACT TTATTTTCT ATAAGGTAGG AATAATATCC ACTTCATTAG CTCATCATGA      240
GGGATAAGTA GGATTGAAA AGATACTTTC AAAGGGCACC TAACTGTGAA GAAGATGCCT      300
TCATTTCAT TCTTTCTTG GCACATTCT TGTATCCAG TCATTCATTA GGACTCCATG      360
TTTATTGAAC ACCTACTCTG TGCCAGGCAC TTTTCTCTGT TCTGGAAATA TCACCATGTA      420
AAAACAAATA GCTGAAGAAT GCCCTGCCCT CATAGAGCTT ACAGACATAG AGCTCGAG      478

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

GAATTCGGCC AAAGAGGCCT AGCGTTCTG ACTTTATTAC TGGTAATTTA TTGCACAGGT      60
TTTCTGTCAT CAAAAAGTA TCTGCTAAAA TAGAGAAAGT TGTGTCTGAA TTCACATTTC      120
CCCCCAACTT CTAATAATAT TTCCCTAAA AAAGAATCCA CTCATCTAAT TTAAAGAAA      180
ATATACTTCT TACACAAGAC AATCCAACT GATGCAAAAT ATTTATTCCA AGTTAGTTAT      240
TTTATGCAGT AGTTTCCCCC TCGAG      265

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

GAATTCGGCC AAAGAGAGAA ATTTAATCT TGAAAGACTT TTCAGGGTAT CTCATTTTTT      60
AGGTGGGGGT GGCAGGTGTA TTTCTTTTT AACAAATAAA AGGCATTAA GTAAAACTAA      120
AATGAAAAAA GTAGGCCTTC TGACATTGTG TACTTGGTGG TTCTGTCCCT CTGCCGTGAA      180
CAAATCTCAT TTTGTACC AAGAACTGTA TGAAAGAAGT AAATCCACCC CTCTCGAG      238

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

GAATTCGGCC AAAGAGGCCT ATGCCTGTGT TGGGTTGACA GTGAGGGTAA TAATGACTTG      60
TTGGTTGATT GTAGATATTG GGCTGTTAAT TGGTGTGTA GAATATTTGA GCACAGGTGG      120
AGTAGAAACA AATCACAAG ACTTTAAGGA GTTGAGGTAT AATGAAAGTC TCACAACTT      180
CAGCTGTCAT GGGAAGAATG GAACCACCA TGAAGGATC ACTCATGTT TCAAGTTACA      240
GAGTGCCTAT GAGAGTGGCC TGATGCCTA CACGAATTAC ACATTGATT TCAAGGTAT      300
AATAGACTAC ATTTTCTATT CTAAACCTCA GCTGAACACC TTAGGCATCC TGGGCCCTCT      360
GGACCACCAC TGGCTGGTTG AGAATAACAT CAGTGGCTGC CCGCACCCCC TCATCCCCTC      420
TGACCACTTC TCACTTTTG CAACTGGA GCTCTTACTG CCTTTCCTGC CCCAAGTCAA      480
CGGCATTCTC GAG

```

## (2) INFORMATION FOR SEQ ID NO:229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

GAATTCGGCC AAAGAGGCCT AAGAAATCAA AATTAAAGCA ATCAAATAAT ACTCACATT      60
ATATAAGAAA TACTTCAATT TACTTTCCAA TGAGTAAAGT TTTATATTTA ATGTTTTAAT      120
ATTTTCATATT TAGTTTCTT GCAATTATTT ACTTTTCTA AAACCTACTT AAATTAGGTT      180
TAAAAGTCTA CTATATATAA TTTGAAATTT TATTCAGTTT GCCTACAGGT GTGTTTTAAC      240
CACTGTGTAC ATAGTATTTA ACGGCTGCT TTTTTTTTT TAATATGGT TCATGNTGA      300
ACATCTGTAT GTTCATACTT TTCTTGACAA AGTTCTAAAG GTTACTGTGT TGAAGCATA      360
TGAACGATTA CTGATAATTT CTATTTTGAG GAACAGGTAT GTCAGTTCTT TCTCTCTGT      420
TGATAATTCT CTCTTTTCCC CTTAGGAATC CAAAAATCCT TGTGGAGTGT CTTACTCCTG      480
ATTTTCGAGG TGATCTCAA GCAATAGAAA AAGTTGCTCT GTCAGGATTA GATGTGTATG      540
CACATAATGT AGAAACAGTC CCATTGCTCG AG

```

## (2) INFORMATION FOR SEQ ID NO:230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

GAATTCGGCC TTCATGGCCT ATCGAGATAC GCTTTCGCGC ACCAGGTACG CCTGGTGT      60
CTTTGTGGTT TTTCCGATTC TTTTGGGGA GTGCGGGGAG TCACAGTTAG AAGGCGGCCG      120
GGTGTGCTG GAGGAAAGTG CTGAGGTCCA GAGCGTAGTC CGAGGGCTCC GAAGTCAGAT      180
TAAAGGGCTC GAG

```

## (2) INFORMATION FOR SEQ ID NO:231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

GAATTCGGCC TTCATGGCCT ACATAATGAT GCTGCCTCAA AACTCGTGGC ATATTGATTT      60
TGAAGATGC TGCTGTCATC AGAACCTTTT CTCTGCTGTG GTAACCTGCA TCCTGCTCCT      120
GAATTCCTGC TTTCTCATCA GCAGTTTAA TGGAACAGAT TTGGAGTTGA GGCTGGTCAA      180
TGGAGACGGT CCCTGCTCTG GGACAGTGGA GGTGAAATTC CAGGGACAGT GGGGGACTGT      240
GTGTGATGAT GGGTGGAACA CTACTGCCTC AACTGTCGTG TGCAACAGC TTGGATGTCC      300
ATTTTCTTT CGCCATGTTT CGTTTGGAC AAGCCGTGAC TAGACATGGA AAAATTGGC      360
TTGATGATGT TTCCTGTTAT GGAAATGAGT CAGCTCTCTG GGAATGTCAA CACCGGGAAT      420
GGGAAGCCA TAACTGTTAT CATGGAGAAG ATGTTGGTGT GAACTGTTAT GGTGAAGCCA      480
ATCTGGGTTT GAGGCTAGTG GATGGAAACA ACTCCTGTTC AGGGAGAGTG GAGGTGAAAT      540
TCCAAGAAAG GTGGGGGACT ATATGTGATG ATGGGTGGAA CTTGAATACT GCTGCCGTTA      600
TACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

GAATTCGGCC TTCATGCGCT ACAGCGCTGC CTTTCTTAT GAAGAAGACA CAAACTTGGA      60
TTCTCACTTG CATTATCTT CAGCTGCTCC TATTATCC TTTCGTCAA ACTGAAGGGA      120
TCTGCAGGAA TCGTGTGACT AATAATGTAA AAGACGTCAC TAAATTGGTG GCAAATCTTC      180
CAAAAGACTA CATGATAACC CTCAAATATG TCCCGGGAT GGATGTTTTC CCAAGTCATT      240
GTTGGATAAG CGAGATGGTA GTACAATTGT CAGACAGCTT GACTGATCTT CTGGACAAGT      300
TTTCAAATAT TTCTGAAGGC TTGAGTAATT ATTCCATCAT AGACAACTT GTGAATATAG      360
TGGATGACCT TGTGGAGTGC GTGAAAGAAA ACTCATCTAA GGATCTAAAA AAATCATCA      420
AGAGCCCAGA ACCCAGGCTC TTTACTCCTG AAGAATTCTT TAGAATTTT AATAGATCCA      480
TTGATGCCTT CAAGGACTTT GTAGTGGCAA ATCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

GAATTCGGCC TTCATGGCCT ACCTTGATAC ATCAGCTGAC CTCATTCCG GATACCTTTT      60
CCCCCCGAA AAGTACAACA TCTGGGCGC CCCAGCCGA AGACAGATCG TCGCTCCCTG      120
GACAATCAGA CGAATTCTCC CCCCCCGC AAAAAAAG CCATCCCCC GCTCTGCCCC      180
GTCGCACATT CGGCCCGC GACTCGGCA GAGCGCGCT GGCAGAGGAG TGTCCGCGAG      240
GAGGGCCAAC GCCCGCTGTT CGGTTTGC GAAGCAGCAG GGAGGTGGG GGCAGCGTCG      300
CCGGCTTCCA GACACCAATG GGAATCCCA TGGGAAGTC GATGCTGGT CTTCTCACCT      360
TCTTGGCCTT CGCCTCGTGC TGCATTGCTG CTACCGCCC CAGTGAGACC CTGTGTCTCG      420
AG

```

## (2) INFORMATION FOR SEQ ID NO:234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

GAATTCGGCC TTCATGGCCT AAGAGATTAA GTGATTTACT CAAGGTCATA TTCCTTGGAA      60
GTAGCAAAAC TTCTGGACCA GATTTCGTAT TCCAAAGGCG GTACTGCTTG TACAACACTC      120
TGAGAAGTAA TTAAGTGGA GCAAAGCAAA AAGAAGTCTA AAAGCAGGTG ATAGGTGTAG      180
ATTTAGATAG TGTAAGGGTA GGCTAAAGTG TTGTAACAAA TGCACCCTCA AGTAGGTAAT      240
GGCTCAAACA CAATAGATGT TCACTTCCCA CATCTCAGAG CAAATTGGGT TCTCCTCATC      300
AGCTAAAGCT TTCCTACATG GGATGATTG GGGAGCAAGA CACTCCATCT ATGGCTCCCT      360
TACCCTCCAA GGCCTTCTTA TTGTCITTAT GTAACCAAGT GAAGAGCTCG AG              412

```

## (2) INFORMATION FOR SEQ ID NO:235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

GAATTCGCCT TCATGGCCTA GGCTTCTTCG GAGCTGTGTA NTCTTAATTT GCTTTGCTGC      60
TGGCTGGCTG ACAGCTGATG GGGGACTCCT CANGACGGAC TCCCTTCCAG ATGCACCCAT      120
CTCCATCCTT CTCAACTCCC CAACCTTTGT CCTCCCCACT CTTCGCTCGC GCGGCGGTCT      180
GAGACCACCA GGACCAAGTT CAGGGGTTTC CTCTCCAGC GAGACTTGGC AGAACAGGCT      240
TTAAAAGCAA AGGAGGCAGC GGAAGACTGT GAATTCCTTT GGACCAATTGA TGATATTTAT      300
CATTGTGCCC AGTTTCTACA AATAAAAGAT GGGTGGATTA TTTTCTCGAT GGAGGACAAA      360
ACCTTCAACT GTAGAAGTTC TAGAAAGTAT AGATAAGGAA ATTCAAGCAT TGGAAGAATT      420
TAGGGAAAAA AATCAGAGAT TACAAAAATT ATGGGTTGGA AGATTAAATC TGTATTCTCT      480
AGTTCTCTAT CTGTTAACAT GCTTAATTGT ATATTTGTGG TATCTTCTCG ATGAATTTAC      540
AGCAAGACTT GCCATGACAC TCCACATCT CGAG              574

```

## (2) INFORMATION FOR SEQ ID NO:236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

GAATTCGGCC TTCATGGCCT AGGCGGGGCC CGGGTTCCCG TTCCCGCGCG AGCCATGCGG      60
TACACGAGA AGGAGCTGCA GGCTCTGTCC CGGCAGCCCG CCGAGATGGC GGCGGAGCTG      120
GGCATGAGGG GCCCAAGAA GGGCAGCGTG CTGAAGCGGC GGCTGGTGAA GCTGGTGGTG      180
AATTTCTCTT TCTACTTTCG GACAGACGAG GCCGAGCCCG TCGGAGCCCT GCTGCTGGAG      240

```

CGCTGCAGAG TCGTCCGGA AGAGCCCGGC ACCTTCTCCA TCAGTTCAT TGAGGACCCT 300  
GAGAGGAAGT ATCACTTCGA GTTCAGCTCG AG 332

## (2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAATTCGGCC TTCATGGCCT AATTGCAAGA TCACGGAATC TCCTGAATCA TTAAGAAAAG 60  
ATAAAATATC ACAAGCATCT TTAGTGTTAT GTGTATTCAG TAATTCCTTG GAGTTGTATT 120  
TATTAAGCTT ACCAGATTTT AAAGGCATAT AAAATGTGGT AAGATATGAG ACACATACTG 180  
AAATATCAGT GCAAAGGGAG AATGGTAGTT GAATGGTCAG AAACGAAAAA GCCTCGAG 238

## (2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCGGCC TTCATGGCCT AGAAGCATTT TTTGTTATTG TGAAACATTT TTATACTTTC 60  
ATTATAAATT GTTGAGCCTA GAGTTGGGCT ATTTGAATAT TTATTATGAT AATCTTTTGG 120  
CTAATGGTAA CAGCATATCT TGTCTAACA AAATTACTGT TAACAGCAAT CGAACTCGAG 180

## (2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 578 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAATTCGGCC TTCATGGCCT ACTGAGATCC AGACCAGCTC CTCCAGACC TCTCCAGAAG 60  
AAGCCATGGG AACCCCTCGT ATCCAGCATT TGCTGATCCT CCTGGTCCTA GGAGCCTCCC 120  
TCCTGACCTC GGGCCTAGAG CTGTTTGTG AAAAGGGTCT GTCCATGACT GTGGAAGCAG 180  
ATCCAGCCAA TATGTTTAA TGGACCACAG AGGAAGTGGA GACTTGTGAC AAAGGGGCAC 240  
TTTGCCAGGA AACCATACTA ATAATTAAAG CAGGGACTGA GACAGCCATT TTGGCCACGA 300  
AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA TAACAATTGT CCAGCACTCT TCACCTCCCG 360  
GCCTGATCGT GACCTCCTAC AGTAACTACT GTGAGGATTG CTTCTGTAAT GACAAAGACA 420  
GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA CCACAGCTTC CACTGTGTCA ACAACCCTCC 480  
ATTGTCCAAC CTGTGTGGCT TTGGGGACCT GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA 540  
ATGGTACAAC TCGATGCTAT CAAGGAAAAC CTCTCGAG 578

## (2) INFORMATION FOR SEQ ID NO:240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

GAATTCGGCC TTCATGGCCT ACATGAATCC ACTCCTGATC CTTACCTTTG TGGCAGCTGC      60
TCTTGCTGCC CCCTTTGATG ATGATGACAA GATCGTTGGG GGCTACAAC GTGAGGAGAA      120
TTCTGTCCCC TACCAGGTGT CCCTGAATTC TGGCTACCAC TTCTGTGGTG GCTCCCTCAT      180
CAACGAACAG TGGGTGGTAT CAGCAGGCCA CTGCTACAAG TCCCGCATCC AGGTGAGACT      240
GGGAGAGCAC AACATCGAAG TCCTGGAGGG GAATGAGCAG TTCATCAATG CAGCCAAGAT      300
CATCCGCCAC CCCCAATCG ACAGGAGACT CGAG                                     334

```

## (2) INFORMATION FOR SEQ ID NO:241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

GAATTCGGCC TTCATGGCCT AGGGCACCAC TGAGTTCAGT ACTTCAAAAT TGCCGTGCTC      60
TACCTCTCCC CAGTGCACAA AAACACTCTC CACACCAAGC TGCTGCTGCT GGGGGATGGA      120
GGGATGGCGT CAGCGATTCA AGACTGTTTT TCCTACCTGT TCAGCACTTC TTTCAGCGAT      180
ATGAAGTTAA ATCCAGTCTT TCCCTGTCTC CAGGCATCAT CGCCATCAAC ATACAGCCAT      240
ACTCCAGGAT TGCCCATCTT CAACATAAAC GGACTCTCCT GGACTCCACT TCCCACATCA      300
GTCACAGCCA CACTTCCTGA GAAAGAAGTC TACTCTTC ATTCACTTTC ATTCACCCAC      360
TGCTCGAG                                     368

```

## (2) INFORMATION FOR SEQ ID NO:242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```

GAATTCGGCC TTCATGGCCT AGAGAAAATA AAGAGTTATA TCAGAAATTT ACAAACATAA      60
CTTTTAAAT TTAAATTGC AAAATATATA TCATACGAAA ATGAAAATTA TAATTCTTCT      120
TGGATTCTCG GGAGCCACAT TGTGAGCCCC ACTTATCCCA CAGCGTCTCA TGTCTGCCAG      180
CAATAGCAAT GAGTTACTTC TTAATCTTAA TAATGGTCAA CTTTGTCCAC TACAACCTCA      240
GGGCCCCACTT AATTCATGGA TTCCACCTTT CTCTGGAATT TTACAACAGC AGCAGCAGGC      300
TCAAATTCCA GGACTCTCCC AGTTCTCTTT ATCAGCTCTA GACCACTTTG CTGGACTGCT      360
CCCAATCAG ATACCTTTAA CAGGAGAGGC CAGTTTGGCC CAAGGAGCCC AGGCAGGCCA      420
AGTTGATCCC TTACAGCTTC AAACACCGCC TCAGACACAA CCAGGCCCCAC GTCTCGAG      478

```

## (2) INFORMATION FOR SEQ ID NO:243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```

GAATTCGGCC TTCATGGCCT ACTTACAGAA CCTATTCACT GGAAGGAAG CCCTCATTAT      60
AATGATTTTC ATTCTTATGT GTGTTTCAGG ACGACTGGGT TTGGATTCAG AAGAGGATTA      120
TTATACACCA CAAAAGGTGG ATGTTCCCAA GGCCTTGATT ATTGTTGCAG TTCAATGTGG      180
CTGTGATGGG ACATTTCTGT TGACCCAGTC AGGCAAAGTG CTGGCCTGTG GACTCAATGA      240
ATTCAATAAG CTGGGTCTGA ATCAGTGCAT GTCGGGAATT ATCAACCATG AAGCATACCA      300
TGAAGTTCCC TACACAACGT CCTTTACCTT GGCCAAACAG TTGTCCTTTT ATAAGATCCG      360
TACCATTGCC CCAGGCAAGA CTCACACAGC TGCTATTGAT GAGCGAGGCC GGCTGCTGAC      420
CTTTGGCTGC AACAAAGTGTG GGCAGCTGGG CGTTGGGAAC TACAAGAAGC GTCTGGGAAT      480
CAACCTCGAG                                     490

```

## (2) INFORMATION FOR SEQ ID NO:244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```

GAATTCGGCC TTCATGGCCT AGAAAAAAGA AACTGTCGTG GATACTGTCA GTGTATATAT      60
TTATGTGGTA CTTGAGAGCC ACCCCAAATT AGATTGACTT TAGATCGTTT ATACAAAAAT      120
AGCTTGAAGA ACTGTTTTTT CCATGGTAAA TGCTTTTGAA TATTAACTTA GTTATGTTAG      180
ATTCTACCT CAGTGGTACT GTCACAGCCA TTGGTTACAT TTCTGAAACC CTTCAGAGTA      240
AGAGTTTTGG TTTTGTGTTT TGTTTGTGTT TGTTTTTGA GATGGAGTCT TGCTCTGTCTG      300
CCCAGGCTGG AGTGCAGTGC AGCAACCCAG GTGGAGTGCA GTGCAACCTC CACCTCCCAG      360
GTTTAAGCGA TCCTCCTAAC CTCGAG                                     386

```

## (2) INFORMATION FOR SEQ ID NO:245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

GAATTCGGCC TTCATGGCCT AGCTTCAGTA GCAAATAAGG ACATCATCTG CTATAACCTA      60
CAAGCAGTTG GACAGATATT CTACATTTCC TCATTCTCTT ACACCGTCAA TTACATCTGG      120
TATTTGTACA CAGAGCTGAG GATGAAACAC ACCCAGAGTG GACAGAGCAC ATCTCCACTG      180
GTGATAGATT ATACTGTGCG AGTTGGTCAA ATGGCCTTTG TTTTCTCAAG CCTGATACCT      240
CTGCTATTGA TGACACCTGT ATTCTGTCTG GGAAATACTA GTGAATGTTT CCAAACTTC      300

```

AGTCAGAGCC ACAAGTGTAT CTTGATGCAC TCACCACCAT CAGCCATGGC TGAACCTCCA 360  
CCTTCTGCCA ACACATCTGT CTGTAGCACA CTCGAG 396

## (2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 514 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCGGCC TTCATGGCCT ACACCTTTCA CTTATCTTAT AGTCACTTAA TTCCTCTACT 60  
 CTTATCATTT GATATTTTCA TTTTATTGTG TATCTCTGTN NGGCCAAATC AATAGATTTT 120  
 GAACAATCTC AACTTTAACC TTTTAAAAAA ATCTAATAGG CCCAGTTTCC TCTCAACAAT 180  
 CTTTGAAGAA CCTTCGAGAA AGGAGAAACA CAGACCTCCC GCTTCTAGAC ATGCACACTG 240  
 TAACCCGGGA AGAGGGAGAA GGCATGGAGA CAACTGATAC GGAGTCTGTG TCTTCCGCCA 300  
 GCACATACAC ACAGTCTTTA GAGCAGCTGC TTAACCTCTCC CGAAACTAAA CTTGGTATGT 360  
 TACTCTGTCT AAATATGTTT TTCTTATTTA ATTTCACTGT CTTATTTAAT TACTANTACT 420  
 CTAAGTTACA TATGCTTTTT NGGGCTGCTC CAATAAAAT TCTTCAATA TTCCACTACC 480  
 TGTTTGTATT AGGTTCTCTA GAGGGACACT CGAG 514

## (2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCT TCATGGCCTA GGTTTTCTGT ACATGGAGAT TAACTGTCT TCCAAAGTGA 60  
 AGAGTTTATT GTTCTAGATC TTGAGCACAA AGGTGGTAT ACGTTAATAA AAAAAATAGC 120  
 AAGGGAAGAA AATCATTTCC TTCATACCAA GTAAGAGAGC ACTTATCATG GTAGGCACTG 180  
 GCTTTGCAAT TATGAGACCA GTAGTAGAAA TAGCTTTAGT TTCCTCAAT TTCTGGAGT 240  
 ATTCTTCAGA CTTTCTTTAC ACTGCTCAAG GTGGGGCGAG TGGCAGGGCG GACCCTGGCG 300  
 ACCTGACGCT GCGGAGGCTC GAG 323

## (2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 423 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC TTCATGGCCT AGGAACAGTG TGTGTTTTTG TGTGTGGCTT GCATTCTCTC 60  
 CTCGGTTTTT GGAGCAGCGT GAGATTATTG CAATGCTACA TTTCCTCCCT CTGCGCCCTC 120  
 CTACCCCATC AATGTCTCAT GGGTGGTGTG ATAGAGGCTA TGGGAGTGAA GACCACTGGT 180



GTTAGTCTGT GTATAGTTCC TGGGGTGTGG CGACTACCAG CTCTGACAGC GGAAGAGAAC	240
TATAGTGTG ATTCCCATTA TTCTCAGTAG GTGTGTTCTA TAAAATTGCT GCGAACACCA	300
AATTAGCGAA TCCTGAACCA TCGTTCCCAG AGGAATAGGG GGTTAGGGTC CTGTGATCCT	360
CAAGTTGCAA CATGTCTTC GACTGATTAA TATGTAACCT TGTTTTATAT GTGCAATCTC	420
GAG	423

## (2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 124 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GAATTCGGCC TTCATGGCCT ACCGAAACCA AATAATTCAA GCACTGCTTA TTACAATTTT	60
ACTGGGTCTC TATTTACCC TCCTACAAGC CTCAGAGTAC TTCGAGTCTC CCTCACCCCT	120
CGAG	124

## (2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC TTCATGGCCT ACATCTATGA CTTTTTAAAC ATGCGGCGTT TTGTGAATAT	60
CATGATAATA ACAAGAGTCA ACAGGCTAAG TGAGAGGAGA GGGATGCTAC GCCTACGCTG	120
CCCCCACCAC GGCCAGCCGG CTTCTGCGCC TTTGGTGTG GATTTTCTTT GTGATTTTAC	180
GGGGTTTGT GTTTTTTTT TCTTGTTTT TGTTTGTTA TTTTTCCTG TCCACTTGAT	240
TTGCATGCAA CACCCACAAA AAGGAAACAC AAAACCCGT CTGCTCGAG	289

## (2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GAATTCGGCC TTCATGGCCT AACTATGAG AGGACCGATT GTATTGCACA TTTGTCTGGC	60
TTTCTGTAGC CTTCTGCTTT TTCAGCGTTG CCACACAATG TCTGGCCTTC CCCAAATAG	120
AAAGGAGGAG GGAGATAGCA CATGTTTATG CGGAAAAAGG GCAGTCCGAT AAGATGAACA	180
CCGATGACCT AGAAAATAGC TCTGTTACCT CAAAGCAGAC TCCCCAACTG GTGGTCTCTG	240
AAGATCCAAT GATGATGTCA GCAGTACCAT CGGCAACATC ATTAAATAAA GCAAAACTCG	300
AG	302

## (2) INFORMATION FOR SEQ ID NO:252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

GAATTCGGCC AAAGAGGCCT ATTTTTTTTT CTGCAAACAC TGTGTATAGT GAGACTTGTT      60
CTACTTTGGA GAACAGGTTA CCTTTTGAAA ATGAGGTTGA GTTCTTCCT TTCTGATGCA      120
TTGATTTTGG AAGATTTTTT TTTCCCCCTT CCCCTCTCCC TCGAG                      165

```

## (2) INFORMATION FOR SEQ ID NO:253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

GAATTCGGCC AAAGAGGCCT AGCTTCTTTG TATAATTAAA TCTGAGTTTT GTTTGAGCAT      60
CTTTCAACAT GTACCATATT TATGACAATT CTCTCCATA GGATCTATCT GTTCTGCAAC      120
AAGTATGAT CTTACAGTAA AATTTTTCAC AAATTCATTA GATTCTATGT CTCTTTTCT      180
GGTAGGAATT TTTGTGCAGG TAGCTATCTC TTGCCCTAGA TTATTCTCCT TGTTTAGCTG      240
CTGATTCTTA AACTGGCCTC TAGATTTCCT GATTCTTCC GGTACAGACT TTCTCTTGC      300
AAGTTCTTCC ATCTCTAATC TTTGAGATTA ATCTCTTTT GAAATGTCCT GCTGCTCTAC      360
TCTTGATGTT CTCGAG                      376

```

## (2) INFORMATION FOR SEQ ID NO:254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

TCTCCAAGGG AAAATAAATG CTTTACTAT CTAGTTTGTG TCTTTGAGAA TTAAGACTCT      60
TTTTTTTTTT TTTCATTCCA GTAGCTTTTG GGGTAGAGTT TGGCTCTTG AGAATTGCAT      120
ACTAATTAAT TTTAGGGGTG ATTGTACAT CATCTCTATA TTCTGAAAC ACAGTAGAAA      180
CAGCCAGCAG TCAGGCAACC ATCTACCATG ACCATTAAAA CATCCCCAAA GTGAAACACC      240
AGATGTGATC TGCTAGATT AGTGGAGGCG GCTGGCTCGA G                      281

```

## (2) INFORMATION FOR SEQ ID NO:255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC	AAAGAGGCCT	AGCTAGNCTT	GCTCAGCTTT	GTGGATACGC	GGACTTTTGT	60
GCTGCTTGCA	GTAACCTTAT	GCCTAGCAAC	ATGCCAATCT	TTACAAGAGG	AAACTGTAAG	120
AAAGGGCCCA	NCCGGAGATA	GAGGACCACG	TGGAGAAAGG	GGTCCACCAG	GCCCCCAGG	180
CAGAGATGGT	GAAGATGGTC	CCACAGGCCN	TCCTGGTCCA	NNTGGTCNTC	NTGGCCCCCN	240
TGGTCTCGGT	GGGAACTTTG	CTGCTCAGTA	TGACGGAAAA	GGAGTTGGAC	TTGGCCCTGG	300
ACCAATGGGC	TTAATGGGAC	CTAGAGGCCC	ACCTGGTGCA	GCTGGAGCCC	CAGGCCCTCA	360
AGGTTTCCAA	GGACCTGCTG	GTGAGCCTGG	TGAACCTGGT	CAAACCTGGT	CTGCAGGTGC	420
TCGTGGTCCA	GCTGGCCCTC	CTGGCAAGGC	TGGTGAAGAT	GGTCACCCTG	GAAAACCCGG	480
ACGACCTGGT	GAGAGAGGAG	TTGTTGGACC	ACAGGGTGCT	CGTGGTTTCC	CTGGAACCTC	540
TGGACTTCCT	GGCTTCAAAG	GCAACCTCGA	G			571

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC	AAAGAGGCCT	ATGCGCAAGG	ATCAAGCCGA	CTACCTGTGC	TGTCTACTGG	60
GACAGCAGTC	TCCGAGCTAC	TCCGTACCTC	CCTCTGCCAG	GTCGTGGAGT	TAGGCCCCAG	120
TCCCTACTTG	TCACTGGTTC	CCACTGTGCT	CCTAACTGTG	CAGCACCTGG	GAGCTCTGGC	180
CTGGGGCTGG	AGGCCCTGGT	AGGAGCTGCA	GTTGGAGGCC	GTTCTGTGCC	CAGCAGCGGT	240
GAGCGGCTCC	CATGGGCCCT	GTGTCTGCAG	GGAGCCAGGG	CTGCGGCACA	TGTGCTGTGA	300
AACTGGCACC	CACCTGGCGT	GCTGCTGCCG	CCACTTGCTT	CCTGCAGCAC	CTCCTACCCT	360
GCTCCGTGTC	CTCCCTCTCC	CCGCGCCTGG	CTCAGGAGTG	CTGGAAAAGC	TCACGCCTCG	420
GCCTGGGAGC	CTGGCCTCTT	GATATACCTC	GAG			453

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTCGGCC	AAAGAGGCCT	ATGTCATGAG	TGAACTTGGC	AATTGCCTTG	TTAAAACCAG	60
TTGGACATTA	TCITCCACAT	TGCGAAGCTA	TACATGTCTG	ATATGTTCTG	AAAGAATAGA	120
ATTTATAGTT	AGATATACTA	TTTTTGATTA	TTTACTCAGA	AGGAGACATG	TAATTATTCT	180
TATGTTGTCA	TGAAAATCTA	TTAAATGCAT	TTATATTTC	CATCAATGTT	ACGAAGTTCC	240
ATTATTATTA	TTTITACAGAG	GGGAAGCCAA	GATACAGGAG	TGGAAATTAC	TTGGCCTATC	300
GCTCGAG						307

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```
GAATTCGGCC AAAGAGGCCT AAGAAGATGA ACAAGCGCCA GCTCTATTAC CAGGTTTTAA      60
ACTTTCGCCA TGATCGTGTC TTCTGCACTC ATGATATGGA AAGGCTTGAT CGTGCTCACA      120
GGCAGTGAGA GCCCCATCGT GGTGGTGCTG AGTGGCAGTA TGGAGCCGCG CTTTCACAGA      180
GGAGACCTCC TGTTCCTCAC AAATTTCCGG GAAGACCCAA TCAGAGCTGG TGAAATAGTT      240
GTTTTTAAAG TTGAAGGACG AGACATTCCA ATAGTTCACA GAGTAATCAA AGTTCATGAA      300
AAAGATAATG GAGACATCAA ATTTCTGACT AAAGGAGATA ATAATGAAGT TGCTCTCGAG      360
```

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```
GAATTCGGCC AAAGGGGCCT ACCTGAAACG GCAGTCCGGT CCCTCCGACA TTGTCCAGCG      60
GAAGGCCTGG GCTTCACACT CTGTGCCTCC CGGCGCTACC TGGCACGATG CCGAGCACAC      120
AGCAGATGCT CAATGAATGC CCAACCAACC CTATACCTGG CTTGGATCTC AAGTCCCCTG      180
GCCGGGGCCT GATGGAAGGC TTTGGGGGCA CAGGAGGCTG CCCCTTGGG CGCCCCCGGC      240
CACCTCTTCG CCCTCGAATC TCAGGCAGCT TGGTCAGGAA CTTCTTCTCC ACGTATTTAG      300
CGTGAATCCA GGCCTCCTTC TCCTGCCTGT GGGAGGGGAG AAGCACGCAG TCTTCCCTCT      360
TCTGTCCAG GGTCCCCCA TTCCCTGGG AGGCTAAACC CATAGCTCGA G                      411
```

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```
GAATTCGGCC AAAGAGGCCT AGGGAGTGTT TCGTTTCTT CTCCGTTTGG CAGTGAAACA      60
CATCTCAGAA AGGTGGAGCT GATCAGAATA ATGTTTCAAGCA TCAACCCCTT GGAGAACCTG      120
AAGGTGTACA TCAGCAGTCG GCCTCCCTTG GTGGTCTTCA TGATCAGCGT AAGCGCCATG      180
GCCATAGCTT TCCTGACCCT GGGCTACTTC TTCAAAATCA AGGAGATTAA ATCCCCAGAA      240
ATGGCAGAGG ATTGGAATAC TTTTCTGCTA CGGTTCAATG ATTTGGACTT GTGTGTATCA      300
GAGAATGAAA CCCTCAAGCT CGAG                      324
```

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```

GAATTCGGCC AAAGAGGCCT AGTGGGGCTG TATTTTAATA CAAGAAAGAC ATTGCTCTAG      60
AACATGGCTC GCCTTTGCTT CAGGGCCTAG CAGTTTATTT TAGCCATAAG GGTAAGGGAG      120
CAGGTCAGAA ATGACTTTTA GTGTAATCCT ATCTGTAATT AAAAATACAA ATGCTGTCAT      180
AAGATCAAAT GTTATCAAAA ATCAGTATTT AAAATTAAAT TTACCCCAA ATTTCCTTCA      240
AAAAAGTTGT AATGTTCTTT TTCAGTGAAG CCTTTGCACT GCTAGAGCTG AAGAATGTGA      300
TCAATCGGCT TGTGAATAA TCCCGCACAG TAGGTATTCC GCTGAAGCCA ACTCTAGCTG      360
GGGGCTCGAG                                     370

```

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```

GAATTCGGCC AAAGAGGCCT AAGAAATAGG ACTATACAAA TTTTCAACTT CTTTGATAT      60
CAGTTTTGGT AAGATGCATT TTTCTTCTGA GAATTTGTTT CATTTGAATT TCCAAATTTA      120
TTAGCATGAA GTTGTTAATA AAAATCTTAT ATTTTACTC AAATTTTGAG ATAGTTGTAG      180
ATTTACATGA AGTTGTAAAG AATAATAGAA AGATCCTGTG TACCTTTTCC CAGTTTCCC      240
CAAAAGTAAC ATTTTGATA ACTCTAGTAC AGTAGCACAA CTCGAG                                     286

```

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```

GAATTCGGCC AAAGAGGCCT AGGCAAACCG TGTACTAAGC ATCAGTGCAG AGATAGTGAA      60
TGAGACACAG TATTCACCAC TTTGAGCAGT GCCAGTCTAG TATTAGAATA TTTTGGCTA      120
AAAAATTATT TTGAAGCATA AAGAAGCTTT TGTTTGCTCT GGTGATTTTC ATAACATATT      180
CACATTCTTA ATGTATTTTT GGTTTTTCAG AAAGTTACTT CTGGCCTGTG TTCTTTCAGA      240
ATATAGGTTG CAGCTTGTTG TAAGTGCAGG AACTATTGAT AGACTGAGTT TAGAAGAAGG      300
GAAACTCGAG                                     310

```

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCGGCC	AAAGAGGCCT	AGGACTTTGG	GGCAGGTGAT	TAAATTTATA	TAGGTACCTC	60
AAGAAAAAGA	ACCTGAATAT	GCTGCATTTT	CTTTCTTTAG	CTTTTACATG	TAGCATTTTG	120
TTTGCTTTT	GTTATTTTGG	TTTGATATA	TGCTTTTGG	ACCCAATAG	ACTGTTGAAA	180
GAAATTTAAA	AATTACTCTT	GTAGGGATAT	AGTATCCTTA	AAAAATAAAA	ATTAATAAAA	240
ATTTAAAAAA	ATTGCTGCAA	TATCTGGCTC	GAAGGTTGCC	CTATATTAGA	ATAATACTTT	300
AGCCAAACAC	ATCAGCTCGA	G				321

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 550 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCGGCC	TTCATGGCCT	TGTGATTCTG	CAAAGGAGGA	ACAATAATTC	ACTGTTTCCC	60
AAACTTATCT	GACCATAGAA	CATATNTCTC	AGAGTATTTT	TCAAGAGTAG	TATTTTCTGT	120
AATATATGAT	GAAAAATAAT	CGTATCGGCC	ATCTTTGTAC	ATAAGGTCAA	AATGTCAGCC	180
AGCCTGAAA	TAAATGCAAG	CCAAAAGGTA	GAGAGATAAG	TGAATAAAGC	TGGCACACTG	240
TCAGTCCGGA	GTACCATGCT	GCATTCTGAG	TCAAGCTCCA	GGAAACTGAG	CTAGGGTTTG	300
TCTCTAAGAA	GAAAAACTGG	AGCGTCCAAA	GCTTCTGGAT	TCCATTTAAT	TAAACCCCTT	360
TTAAATTAAA	TCCTTGTAAC	TGAAGAGTAT	CGGTGGATGA	AGAAAAATA	GTCTCACATG	420
TCTTCATTTT	CATCCTTGGC	TCAGTACAGC	TCCAGTTCCA	TTATTCTTAA	ACATCTATTA	480
ACATGATTGC	TAAATAATTA	CACAGGCTAA	CTGCCAAGCA	TTTTTCACAG	GAAGCAAGGC	540
ACTGCTCGAG						550

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC	TTCATGGCCT	AGTTAAGTGG	GAAGTTAAAT	GGCAAGTACT	AGAATGCCAC	60
CTATGGCAAG	CACTAGAATG	GTCTAGGTGT	GAAATGAGGG	AGTAATGTCA	GGGAGTCAAG	120
GTGGCCATCC	ATAGCAGTGA	TTCTTATCTG	GGGTAGGGGG	TGAATTTTAC	GTGGAGGGAG	180
GTCTCTGGAC	ATGGACCCCC	AGGCAGGGCT	ATCCAATCAT	CTGAGGGGTG	AGCAGTGTTT	240
AGCTCAGTAA	AAGTAAGGGA	AAAAAATAG	CAGTCTCTAA	AAGGAACATA	GAGCGCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GGGGAGAGCA TCAGGAAGAA CAGCTAATGG ATGCTGGGCT TAATACCTAG GTGATGGGAT	60
GGTCTGTGCG GCAAACACCA TGGCACAAGT TTACCTATGT AACCTGCACA TCCTGACATG	120
TACCCCTGAA CTTAAAATGA AAGTTGGAGA CCAAAAAACA AAACACCATA AACTACAAA	180
ACTTCTTAAA CAATAAACTA GTAGAAAATT TCTAAAATAT ATAATTCAAG AATTATATAA	240
GAGCTCTTTT TATATGTAAA TATAAATTTA AATACAAGAG AAACATCTAA AACAGGTTGC	300
TTCTGAGAAA CGTGACTGGT TATTAAGAAG AGGTATATAG GGGCTCACTC GAG	353

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CATTATTTAA CCTTTTAAAC AATCAAGAGA TTGCTTTTTA AATTGTCTCT AAAAAGGTTT	60
GATTTTITAC GAAAGAGAGA GCACTTGAAT ATATCTTTAT GTACCACCGT GTCTCTTTTT	120
GTTAGATTTT TCATCTGTGG GTATAATATA AAATATTCTT AAAATGAAAG CTTTACGCTT	180
GTGTTTGAGA CTAAGCAACT TGCATGTGT CATGACCCTT CTAATACCAC AAACCCTCGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCGGCT TCATGGCCTA CACTCAACCA CTGAAAAAGC TGAAATCAA TGTTTTTAAG	60
GTTCAACAAGT GTGCCGTGTG TGGCTTCACC ACCGAAAACC TGCTGCAATT CCACGAACAC	120
ATCCCTCAGC ACAAATCGGA TGGTTCTTCC TACCAAGTCC GGGAGTGTGG CCTCTGCTAC	180
ACGTCTCAGC TCTCTCTGTC CAGGCACCTC TTCATCGTAC ACAAGTTAAA GGAACCTCAG	240
CCAGTGTCCA AGCAAAATGG GGCTGGGGAA GATAACCAAC AGGAGAACAA ACCCAGCCAC	300
GAGGATGAAT CCCCTGATGG CCCCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GCGGGCACCA	TTTCCAGTAT	GTACCAAACC	AAAGCCGTCA	TCATTGCAAT	GATCATCACT	60
GCGGTGGTAT	CCATTTTCAGT	CACCATCTTC	TGCTTTCAGA	CCAAGGTGGA	CTTCACCTCG	120
TGCACAGGCC	TCTTCTGTGT	CCTGGGAATT	GTGCTCCTGG	TGACTGGGAT	TGTCACTAGC	180
ATTGTGCTCT	ACTTCCAATA	CGTTTACTGG	CTCCACATGC	TCTATGCTGC	TCTGGGGGCC	240
ATTGTTTCA	CCCTGTTCT	GGCTTACGAC	ACACAGCTGG	TCCCGGGGAA	CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GCCAGACTAC	CACAAGCCCC	ACCCACACTA	TGCCAAGCCC	TACCCATACC	ACAGCAAGCC	60
CCACTCATA	TTCCACAAGC	CCCACCCATA	CCCCACAAG	TCCCACCCAC	AAAACCACTA	120
TGTCACCTCC	CACCACTACA	AGTCCTACCC	CCAGTGGTAT	GGGCCTAGTC	CAGACTGCCA	180
CAAGTCCCAC	CCATCCTACC	ACAAGCCCCA	CCCATCCAC	CACAAGCCCC	ATCGTTATAA	240
ATGTAAGCCC	TTCCAATTCT	CTAGAACTTG	CTACCCCTCT	CAGCCCTCC	AAACACTCAG	300
ACCCACCCCT	CCCAGGCAAT	GACTCCCTTC	CCTGTAGTCC	CCCAGTCTCC	GATTCTCTACA	360
CTCAGGCAGA	CCCTATGGCC	CCCAGAACTC	CCCACCCAAG	TCTCGAG		407

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ACTGAGCTCA	AGGACCCCTC	CAAGAAGAAG	ATGCAGCACA	TCTCCAACCT	GTCCATCGCT	60
GTCATGTACA	TCATGTACTT	CCTGGCTGCC	CTCTGGGCT	ACCTCACCTT	CTACAACGGG	120
GTGGAGTCGG	AGCTGCTGCA	CACCTACAGC	AAGGTGGACC	CGTTTGACGT	CCTGATCCTG	180
TGTGTGCGCG	TGGCCGTGCT	GACAGCAGTC	ACGCTCACAG	TGCCCATCGT	TCTGTTCCCG	240
GTGCGCCGCG	CCATCCAGCA	GATGCTGTTT	CCAAACCAGG	AGCTCGAG		288

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTCGGCC	TTCATGGCCT	AGTCAAGCTA	GGTAAGCTAA	AAAGAAGAAA	ACCTGGTTAC	60
AGCCCGGTGA	ATTGATTTTT	TTCCAGCCGA	GAAATAGATA	TTTCTCTCAC	ATATATTTGG	120
AAAACTTTAG	TCATCTTCAT	AAAACTTAAA	AAGTTACCTA	AGCACACACA	GCAAGTTTCT	180
CCTTTCTTCC	TTTTCCACAC	CCTTACCACT	TCACTATGTT	TCTACCAATC	CAGTCCCCAG	240
TTGCCAATGA	TGTTGCTCTC	ACATGAATTT	ACTGCATTCC	CTTCTGGTTC	CCCAGAAGGT	300
CTTGAAGAAA	GAGGTTTCAGA	CTAGTGGACC	CAAACAGAAT	TTCTTGGCTG	GTGATACTCA	360
GATTGTGTTT	AGAGCCTGGT	ATGAAGAAGG	GGCCAGGTGT	AAGAAGTAGT	TAATCAACTG	420
CACGTTGATT	TCAGGCTGAA	TATTCAACCA	TCTGCAGCCA	CCCGTCTCTA	AAAGTCTAGC	480
TGAAGCACAA	TTGATTGTGC	CATAGAATGA	GCAAACGCTT	GAAAACACAA	GCTCGAG	537

## (2) INFORMATION FOR SEQ ID NO:274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CGGAGCTCGT	GTTTAAAGG	ACCAAATAGA	AGTTTACCAG	GAGAGAAGTG	ACAGAAGTGC	60
TGTCTAGATA	GAGGAAGGGC	ACACACAGAT	GCAAGCATGT	GCAGAAATGA	GCAAACCACT	120
GAGACGCTGC	CTTGAGCTCT	GTGTCACACT	GCTATGTTGC	AGCCTGGGAG	GCTGTTCCCA	180
GTTGAGCCCT	TCGGAACCAG	CCATGAGATG	GCACGGGTAC	GCGGAAGGGA	GCAGTCTCCA	240
TGGCTGGGTG	GTGATGGGGG	CTTCTCGAG				269

## (2) INFORMATION FOR SEQ ID NO:275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GATGGCTCCC	CAGAGCCTGC	CTTCATCTAG	GATGGCTCCT	CTGGGCATGC	TGCTTGGGCT	60
GCTGATGGCC	GCCTGCTTCA	CCTTCTGCCT	CAGTCATCAG	AACCTGAAGG	AGTTTGCCCT	120
GACCAACCCA	GAGAAGAGCA	GCACCAAAGA	AACGGAGAGA	AAAGAAACCA	AAGCCGAGGA	180
GGAGCTGGAT	GCCGAAGTCC	TGGAGGTGTT	CCACCGACG	CATGAGTGGC	AGGCCCTTCA	240
GCCAGGGCAG	GCTGTCCCTG	CAGGATCCCA	CGTACGGCTG	AATCTTCAGA	CTGGGGAAAG	300
AGAGGCCAAA	CTCCAATATG	AGGACAAGTT	CCGAAATAAT	TTGAAAGGCA	AAAAGCTCGA	360
G						361

## (2) INFORMATION FOR SEQ ID NO:276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

GCCACAATAG CGGGATTGAT CTCCTTAGGA CCTATCTTTG GCGTTGCCAG TTCCTTTTAC	60
CTTTTGTGAG TTTAGGTTTG ATGTGCTTTG GGGCTTTGAT CGGACTTTGT GCTTGCAATT	120
GCCGAAGCTT ATATCCCACC ATTGCCACGG GCATTCTCCA TCTCCTTGCA GGTCTGTGTA	180
CACTGGGCTC AGTAAGTTGT TATGTTGCTG GAATTGAACT ACTCCACCAG AAAGTAGAGC	240
TCCCTGACAA TGTATCCGGT GAATTGGAT GGTCCTTCTG CCTGGCAGAA CTCGAG	296

## (2) INFORMATION FOR SEQ ID NO:277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTGCGCC TTCATGGCCT AGGATGTAGA ATCCTGCTTA TCTGTGAAAT GCAGTTGACA	60
CATCAGCTGG ACCTATTTCC CGAATGCAGG GTAACCCTTC TGTATTATTA AGATGTAAAA	120
AATGCGGGAG ACTTGAGAAG AAAGGCCATG GAAGGCACCA TCGATGGATC ACTGATAAAT	180
CCTACAGTGA TTGTTGATCC ATTTAGATA CTTGTGGCAG CAAACAAAGC AGTTCACCTC	240
TACAACTGG GAACAATGAA GACAATGAAC TCGAG	275

## (2) INFORMATION FOR SEQ ID NO:278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TCGTTCCCTT CATCTCTTCC CTGCCCAGAG CAGGGACTCT CTCCATATAA ACAAAGGAA	60
AACCACTGGC CAGGGTATGG TCAATACCTC AACATATCCA GACATCACAG CACCAGAACA	120
CCAGTATGTA TATTCCACAA GTACTCGAG	149

## (2) INFORMATION FOR SEQ ID NO:279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GCAATCAGAT AAAGAAAGAC CTGGCTGACA AGGAGACACT GGAGAACATG ATGCAGAGAC	60
ACGAGGAGGA GGCCCATGAG AAGGGCAAAA TTCTCAGCGA ACAGAAGGCG ATGATCAATG	120
CTATGGATTC CAAGATCAGA TCCCTGGAAC AGAGGATTGT GGAAGTGTCT GAAGCCAATA	180
AACTGTCAGC AAATAGCAGT CTTTTTACCC AAAGGAACAT GAAGGCCCAA GAAGAGATGA	240

TTTCTGAACT CGAG

254

## (2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 327 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GACAGCCTGG AAGTTTGGAG ACCCTGACAC ACCCACCTTC TCACCTGGGC TCTGCGTATC	60
CCCCAGCCTT GAGGGAAGAT GAAGCCTAAA CTGATGTACC AGGAGCTGAA GGTGCCTGCA	120
GAGGAGCCCG CCAATGAGCT GCCCATGAAT GAGATTGAGG CGTGAAGGC TGCAGAAAAG	180
AAAGCCCGCT GGGTCTGCT GGTCTCATT CTGGCGGTTG TGGGCTTCGG AGCCCTGATG	240
ACTCAGCTGT TTCTATGGGA ATACGGCGAC TTGCATCTCT TTGGGCCCAA CCAGCGCCCA	300
GCCCCCTGCT ATGACCCCTG CCTCGAG	327

## (2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GCCTGGAACC TGATTCTCCT GACCGTCTTT ACCCTGTCCA TGGCCTACCT CACTGGGATG	60
CTGTCCAGCT ACTACAACAC CACCTCCGTG CTGCTGTGCC TGGGCATCAC GGCCCTTGTC	120
TGCGTCTCAG TCACCGTCTT CAGCTTCCAG ACCAAGTTCC ACTTCACCTC CTGCCAGGGC	180
GTGCTCTTCG TGCTTCTCAT GACTCTTTTC TTCAGCGGAC TCATCCTGGC CATCCTCCTA	240
CCCTTCCAAT ATGTGCCCTG GCTCCATGCA GTTTATGCAG CACTGGGAGC GGGTGATTTT	300
ACATTGTTCC TGGCACTGA CACCCAGTTG CTGATGGGTA ACCGACGCCC GCTCGAG	357

## (2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GCGGGCTGCA GAATGATAGA CGAGCTCAAC AAAACGCTGG CCATGACCAT GCAGAGGCTG	60
GAAAGCTCTG AGCAGCGGGT CCCCTGTTC ACTTCTTACC ACAGCTCTGG GTTGCACTCG	120
GGTGATGGGG TCACCAAAGC AGGACCTATG GGCCTTCCAG AAATAAGACA AGTGCCAACT	180
GTGTGTGATT AATGTGATGA CAATAAAGAA AATGTGCCTC ATGAGTCAGA CTACGAAGAC	240
TCTTCTTGCC TGTATACAAG AGAAGAGGAG GAAGAGGAGG AGGACGAAGA CGACGACGAA	300
CTCGAG	306

## (2) INFORMATION FOR SEQ ID NO:283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

AATCAATCAA CTAGGCATAT GACACAGTAG TCCATTATAA AAGAAGACAT ACATCCAGCA      60
CCATCAACTA ATTCTTAAGA TAAGTTATCT GGGAAAATTG AAGAACAAAT AAATTCAACG      120
AAATACTGTA AAGTGAACGA AGACATAAAA CCAAAGAAAA CTGAGGCCAT TTCTGCCAAG      180
AAAGGAACAG CAAAGAGTAA AGATGAAAAA TATTCTAAGA TAATACCAGA AAAAGATAAT      240
TCCTACATGG ACAAAGATGA GCATGGTTCA TCCTCTGAAA GTGAAGATGA AGCGCTGGGT      300
AAATATCATG AGGCCTTATC CAGAACACAC AATTCGGAC TACCACTCGA G              351

```

## (2) INFORMATION FOR SEQ ID NO:284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```

AAGTTAAAGG TATTAAATAA ATGAGTTTCT CCTTAATTTT GTTAATGCTC TTTTAGCTAA      60
TAAGACTTTT TCTAGAGTGA CATATTTTAA TCTGTTTCAT TTTTATTTT TCCTTTGGTT      120
TTATATTTT AAAAGCCATT ATATCCCTCC CACTGGTAAC ATACACATAC ACAGACACAC      180
ATCTATTTCA AATGAATACT TACTACTTTA TCATTTTCAG TCTTAATTGT ACT              233

```

## (2) INFORMATION FOR SEQ ID NO:285:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

GCGGCGCCGC AGCAGTTCCA GGAAGGATGT TACCTTTGAC GATGACAGTG TTAATCCTGC      60
TGCTGCTCCC CACGGGTGAG GCTGCCCAA AGGATGGAGT CACAAGGCCA GAATCTGAAG      120
TGCAGCATCA GCTCCTGCCC AACCCCTTCC AGCCAGGCCA GGAGCAGCTC GGACTTCTGC      180
AGAGCTACCT AAAGGGACTA GGAAGGACAG AAGTGCAACT GGAGCATCTG AGCGGGGAGC      240
AGGTTCTCCT CTACCTCTTT GCCCTCCATG ACTATGACCA GAGTGGACAG CTGGATGGCC      300
TGGAGCTGCT GTCCATGTTG ACAGCTGCTC TGGCCCCTGG AGCTGCCAAC TCTCCTACCA      360
CCAACCCGGT GATCTTGATA GTGGACAAAG TGCTCGAG              398

```

## (2) INFORMATION FOR SEQ ID NO:286:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
GAATTCGGCC TTCATGGCCT ACACCCAGCC AATTTTTTTG TATTTTGTAGT AGAGACGGGG      60
TTTCACCATG TTAGCCAGGA TGGTCTCTAT CTCTGACCT CATGATTGTC CCGCCTCGGC      120
CTCCAAAAAA AGAACATTTT ATATTTGAGT GCTATTTCTT TTGCGGCACC AAAACTTTAT      180
AACACACTGC CTTCTGAATT TTTTTTTTTG GTTCTGCTC AGCTCATGT TAATCATATT      240
GTTCCCATGT ATGTCATGAG TTATTTTCTT CTTAGTCTTT TCAAAATTTT CTGTCTTTG      300
ACTTTTAACA GTTTAATTGT AACAGTGAT ATCTTTAAAG TTAAATTCAT GCTTGGAAT      360
TTTATAAGA GCCACAAAGG CCTTCCTCTG TGTTTTGTG TTGTTTGTG TTTGTTTTC      420
ATTTTGAGA CAGGCTCTCA CTGTCCTCA GTGGCTCTCG AG      462
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
TGGACAGTCT AGAAGATGCT GTGGTGCCCC GGGCTCTGTA TGAGGAGCTG CTGCGCAACT      60
ACCAGCAGCA ACAGGAAGAG ATGCGCCACC TCCAGCAGGA GCTGGAGCGG ACTCGGAGGC      120
AGCTGGTACA ACAGGCCAAG AAGCTCAAGG AGTACGGGGC ACTTGTGTCT GAAATGAAGG      180
AGCTCCGTGA CCTTAACCGG AGGCTCCAGG ACGTGCTGCT CCTGAGGCTT GGCAGCGGTC      240
CCGCCATTGA TCTGGAAAAA GTAAAGTCAG AATGTCTCGA G      281
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
AATGGAAGTG CTGACACAAT ACTCGTGTA CTGTGTGGAA CCGCATAATC CCAGCAATGG      60
CACATTGAAG GAATGGAGGG AATCCAATAT TTCTGCCTCT GACATAATTT GGGAGAACCT      120
AACTGTGTCA GAATGCAAT CATTCATGAG AGAGTATGTT GGACGGGCCT GTGGCCATGA      180
TCACCCATAT GTTCAGATG TTCTATTTTG GTCTGTGATC CTGTTCTTTT CCACAGTTAC      240
TCTGTGAGCC ACCCTGAAGC AGTTCAAGAC TAGCAGATAT TTTCCAACCA AGGTTTCGATC      300
CATAGTGAGT GACTTTGCTG TCTTTCTTAC AATTCTGTGT ATGGTTTAA TTGACTATGC      360
CATTGGGATC CCATCTCCAA AACTACAAGT ACCAAGTGTT TTCAAGCCCA CTAGGCTCGA      420
G      421
```

(2) INFORMATION FOR SEQ ID NO:289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

AAGCCAATGG CTGGTCGTGA TCCTGAATGC CAACGCACAG AAATGATTAA GAAAGAAGAA      60
GAACGTTTGA GGGCTTCCAT ACGTAGGGAA TCTCAGCAGC GCCGAATGAG AGAGAAACAG      120
CACCAGCGGG GGCTGAGCGC CAGTTACCTG GAACCTGATC GATACGATGA GGAGGAGGAA      180
GGCGAGGAGT CCATCAGCTT GGCTGCCATT AAAAACCGAT ATAAAGGGGG CATTGAGAG      240
GAACGAGCCA GAATCTATTC ATCAGACAGT GATGAGGGAT CAGAAGAAGA TAAAGCTCAA      300
AGATTACTCA AAGCAAAGAA ACTTACCAGT GATGAGGTAA GACCAAATTT ATTCAATTCT      360
AGGGGTTTAT CCTGTACTCA GGAGCCAAC TCTTTGAATG AAAASCTCAC ACTCGAG      417

```

## (2) INFORMATION FOR SEQ ID NO:290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

CAAGCATACA ATCAACTCCA AGCTCGGTAT CACCTGAGCC CAGGAAGTGG AGGCTGCAGT      60
GAGCTATGAT CAGTAAACAA CAAGACAGGT TCACTGGCTC CCATCCCAAC CCGGACCAGC      120
TCCCTAGTAT AACAACTCAC ATGCATGTGG ACTATACCTT TACAGCCTTC TTCTGTGTGT      180
TTATGTGCAT ATATGTAGCC ATAGGAAAAA AAATCAAAT CTTTGTGTGT TCTTTCTTAT      240
TTTTTCAAT ATTACCTG CCCCATCTC TTTCCTTCT CTTCTAGTA CTCCCATTGC      300
ATGCAATTCT CGAG                                     314

```

## (2) INFORMATION FOR SEQ ID NO:291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

GTGTATGTGG GGGTAAGTG TGTGTGTGTG CGTGTGCGTG TATGTGCACG TGTGTGTGT      60
GTGCGCCTGC ACACGGAGAG CCCACTCATA CGTAGCAGAA AATCAAATGG CCCCAAATCA      120
GAAACATGGC GCATGTGAGC ATGCCACTTC TTGTGTGCCT GTGACTGTTC AGAATGTACA      180
CGGCCCTGCA GCTCCGAAG GCCAGCTCTG CTGCAACCCC TCCTCTGTCC AACACAGTCC      240
TCACTGGTGT CTTTCTCTCT TCAAATCTAC AGCATTTCTG ATCTCTGCAA ACAATTTAAC      300
CCAAAACCAA GTTCTGGCTG ACAAGGCTAC ATCTGTGTTT TTGTGCGTGA TTAGCCTCGA      360
G

```

## (2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```
GCGATTGAAT TCTAGACCTG CCTCGAGTCG ATGCACCGAA AAGGGTGAAG TAGAGAAATA    60
AAGTCTCCCC GCTGAACTAC TATGAGGTCA GAAGCCTTGC TGCTATATTT CACACTGCTA    120
CACTTTGCTG GGGCTGGTTT CCCAGAAGAT TCTGAGCCAA TCAGTATTTT GCATGGCAAC    180
TATACAAAAC AGTATCCGGT GTTTGTGGGC CACAAGCCAG GACGGAACAC ACTCGAG      237
```

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```
GAATTCGGCC TTCATGGCCT ACTTTATTTT TTAAATTATT ATTAGTATTA TTTTGAGACT    60
GAGTCTTGCT CTATCACCCA GGCTGGAGTG CAGTGAGCTG AGACTATGCC ACCGCACTCC    120
AGCCCGGGCG ACAGAACGAG ACTCCATCTC NAAAAAAAAA AAAAAAATCT ATGTTTCATGC    180
CTNACACCT GTTCTGCAC ATAGCTGTGC AGTATATTCT TCTTCTAAGC AACGACCCAG    240
TGAAGATCCA AACAAAAGTT CACAAATATG TAGTTATCCA AGGCACCTCG AG              292
```

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```
GAATTCGGCC TTCATGGCCT ACAATCTTTT AACTTTGGGG GTCACAGTTT TAGCCACCTT    60
TCGGGGGGTG ACTGGAGCAG TAGGAGGTGT GGGGTCATT TATGAATATA ATAAAATGGA    120
GCTGACTGTA CTCGAG              136
```

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

GAATTCGGCN TTCATGGCCT AAAATAACAC ACAATTAGTA TAGAAAAATT GCAAACACAG      60
ATAAAAGTCC TTTCCCTGTG AATTTCTGAA TGCACCTTTG AATATTCACA TCTTACTGCC      120
AAAATGAGAT TGTCTTGTGT GCCGTTCTGG AATTTGCTTT TTTCCAGCTT ACATGTTCTA      180
GGTCCTTCCA GATCAATAGC TGCACCTCCCT CCTTCCTCTG CTGGTTTCTC AGCTCGATGG      240
GCTGTAAGTG GCATTACTCT CGAG                                         264

```

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

GAATTCGGCC TTCATGGCCT ACAACCTCAT AAATCTCATT CTTAATTTC A CTCTAGGACA      60
GAATTATGT AGCACCTGTG TTCTGTTATT TTAGATTCAT TTTAACTTAC CTAGACACGG      120
GTA CTGTGGT AGTTGTAGAG GTACAGATGT TGAGTTCCCA TCCTCCTGGC TTAATGTCAC      180
TGGGGTTATT AATACACTTC ATAAGCATTT TAGGGACACC TGCTGTCTGC TCAACCCCCA      240
GCAAAC TCGA G                                         251

```

## (2) INFORMATION FOR SEQ ID NO:297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

GAATTCGGCC TTCATGGCCT ACATCTGGTA AATTTTCTT TCTGCC TGAG GAACACCCCTT      60
TAGCATTTAT TTAGTCTGCT GGTGACCAAT TCTCATATTT TGTTTGTCTG AAAAATACCT      120
TTATTTTGT TTAATCTTG AAAGATATTT GCACTGGTGT GATTGGATT C ATGATTGCTT      180
ATTATTTTCT TTTTCTTTT TCTTTTGTGA GACAGAGTCT CGCTGTGCGC CAGGCAGGAG      240
TGCAGTGGCC CGTACTCGAG                                         260

```

## (2) INFORMATION FOR SEQ ID NO:298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

GCTCTGAATC TATTTTCTAG GACATTTT TCCCATTTAG ATTAAGCCAG AGAGAGCCCT      60
TTCTTGCCTC CCAAGAGTTT TTCTTTGTGT GACTGTTGGT ATTCTGAACC TCTTGGATTT      120

```



GATGCCTGGA ATTGTCCTAG AGACTCTCCT GATTCTGTG TCATTCTTTG ATTTACCCT 180  
 GGGGAGCTGG GGAAGAGATA CCTTCCCATG GCATCACTTG TTAAGAGTGG ATCCCCCTTC 240  
 CCCCTTTCCT TCTGTCCCC TCGAG 265

## (2) INFORMATION FOR SEQ ID NO:299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAATTCGGCC TTCATGGCCT ACCAAAACAA AAGAAGAAAT CATTCACTC ATGCTTAGAA 60  
 AGATGTCAAG AGGATGGAGG ACTCACATTC TGTTAACTCT TCTGCCTGTA ATATATGCTT 120  
 TAAACACTAA AAATGATGAG CATGAATCTG CAATTCAAGC CCTCAAAGAT GCTCATGAAG 180  
 AAGAAATTCA ACAAATTCTT GCTGAAACAA GAGAAAAAAT ATTGCAGTAT AAAAGCAAAG 240  
 TAACAGAGGA GCTAGACCTT AGAAGAAAGA TTCAAGTTTT AGAATCATCA TTAGAAGATC 300  
 ACAATCTCGA G 311

## (2) INFORMATION FOR SEQ ID NO:300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GCGATTGAAT TCTAGACCTG CCTCGAACTC GTGGCCTCAA GTGATCCACC TGCCTCACCC 60  
 TCATCACCTG CCAAGTCCTA CCCATTCTAA CCTGATAGC TCTTAAATCA GGTCTTTCCA 120  
 CCTCAACCTC ATTATCACTG CTCTAGAGCT CAAGCCTTCA GTGTCCTTTC ACTTCCTGAA 180  
 TTTACTGTCT TAGTGCTCTT GCTCACATTG TATTCTNTGC CCAAATGCT CTTACCACTC 240  
 CCNTTCTTTC TCGAG 255

## (2) INFORMATION FOR SEQ ID NO:301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAATTCGGCC TTCATGNCCT ACTTGGATTT ATCACAGTAG CATTGTCTT CAATCTGTGT 60  
 GTTAACTAGA AATCAAGGAA AGACATGAGG AGATTGTCT ACTGCAAGGT GGTCTTAGCC 120  
 ACTTCGCTGA TGTGGGTTCT TGTGATGTC TTCTTACTGC TGTACTTCAG TGAATGTAAC 180  
 AAATGTGATG ACAAGAAGGA GAGATCTCTG CTGCCTGCAT TGAGGGAGAT CCGCACGCAG 240  
 CTGGTGGAGC AGTTCAAATG TCTGGAGCAG CAATCAGAGT CGCGACTGCA GCTGCTTCAA 300  
 GACCTCCAGG AGTTTTTCCG CCGGAAAGCT GAGATTGAGC TCGAG 345

## (2) INFORMATION FOR SEQ ID NO:302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

GAATTCGGCC TTCATGGCCT AATCCTCCAG ATTATTATGG ATATGAAGAT TATTATGATT      60
ATTATGGTTA TGATTACCAT AACTATCGTG GTGGATATGA AGATCCATAC TATGGTTATG      120
AAGATTTTCA AGTTGGAGCT AGAGGAAGGG GTGGTAGAGG AGCAAGGGGT GCTGCTCCAT      180
CCAGAGGTCG TGGGGCTGCT CCTCCCCGCG GTAGAGCCGG TTATTACAG AGAGGAGGTC      240
CTGGATCAGC AAGAGGCGTT CGAGGTGCGA GAGGAGGTGC CCAACAACAA TGATCTCGAG      300

```

## (2) INFORMATION FOR SEQ ID NO:303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

GAATTCGGCC TTCATGGCCT AAAAAAAGA AGTTTATTTA AAGAACTCT ATAAGAGCAG      60
CTTGGATTTT ATATCTTTAG ATCCAGAGTT TTTACTTTTC TGGAATTAAA TATAATTGTT      120
TGGAATTTAC TCTTTATTGT TGAATTTTAA AGCGTGAATA AAGTAGTGCT TCTTAAGATA      180
ATTGTCATGT GTTTTGTGTT TGTTTGTGTT TGTTTTTGG TGCTGAGTGT TGCTCTGTGC      240
CTCAGACTGG AGCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:304:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

GAATTCGGCC TTCATGGCCT ACAATTCCGA TAAAGTTTAA GGTGAGCTGA TGAAGAACAC      60
TCAAACCAAA GTCGCCCATT GGAGGAGCGC CCTACCTCAC AGGAATAGGC CTGCATTATT      120
AGTATACCTT CTTCAATCAG TTATTGTTAT TCTTATGGAA ACAACCCATG GGAAATGTAG      180
CCTTGGCATG ACTGTATCAA TGGATTGAGA GAGCAGTAGC GGGGACCCCC CCAGTCAATT      240
ACGTTCCACA GCAAGTCTCG AG

```

## (2) INFORMATION FOR SEQ ID NO:305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC TTTCATGGCC TAAATCTCAT AAATAGAAAG NAAAATAATC TAGAAATTTT	60
TCAAAGCTAG TACTCTTTCT CCTTATAAAT GTACACAATT TTAATCTTTT TACAAATTTA	120
TTTAACTGTA CCTACTGTAC TTATTGTAGA TTCAATGACG CAGTTAAGTC ATCACCCTAAG	180
GATTATGAA TTTGAGATTA CTGACCTGTT TTCTTCATAT TGCATTACA TCAATATTTG	240
TGAATTTGTT GTTCAGCTTT TCATTCAAAC AAAAAATATT CCCCCTAAGAA AACTCGAG	298

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GCGATTGAGT TCTCCCTGCT GGTTCCTTTG AATCACACCA AATGAATGGC TTGCTACTGT	60
TCCCTCACAC CTTCATATTG TCCATGGTTT TTCCACCTC CTTAGCTATA CAGCTGCTGT	120
TCCTCCTGCC TAAAATGTCT GAACATTCCC TCAGTGTTCA GCTCAGCCCA CATCTTACAT	180
CTTCCCTAAG GATGTTTTTC TGCTGCTATC ATTCATTTTC TTCCTATGAG TTCCTCTGTT	240
ATATTGCGCC ACCAGAATC GAG	263

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCGGCC TTCATGGCCT AGCCCCGACT AGCTTTGCC TAATCCTTC ATCAAAGAC	60
CCCCCGCCAG CTTCCACAC CTCATACGCA GCCACATCTG CCCTATTCTC CATGCTTTCC	120
AGCTTGCCCTG CCCTTCCTCA TCTCTCCCTG CCTGTGCAGA CCTCCACCCT TCTTCTCTCC	180
ACCCCTCCAT CCCCCAATGC TTGTAGACCT TCCATTCATT CCGTCTCATC GTGCGTGGTC	240
TCTGATCGTC CATCACCTGA CCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC TTCATGGCCT AGCCAAAATC ACAAGAAAAA TAACTTTGAC TTTGAAAACA	60
AATAAGTTAG AAATGCAGTG TTTGCACTTC GTGGTTTATG TTTGCTTTGG TGGCCTCTCA	120
TTCCCACTTA GCCTCAGTCT CCAGGGCCTG GGCTCCACCA AGGAAGACTC CATCTGCTCT	180
CTCTATTTGC ACACTGGGAA CTTTTTCCC CAAGGTACAG GATATGATTC AGGGTTTATG	240
GATGACCTCC CACCCCTCGA G	261

## (2) INFORMATION FOR SEQ ID NO:309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCGGCT TCATGGCCTA CCTATTCCCA AACTTTAAAT GTTGTCTACC AAATACTGAC	60
AAATTATGAAA ATTCTACCAG TAGAACACAC CTCCTTTTG AGCTCCAGAG CACATGCTTG	120
ACATCTCATA TTAGAAAGAA TCTTGATTTC CCCTCCAGTC TAGTCTTTCA TGTTTTGT	180
TTCTTTGTGA GAGTCTCCCT CAGCCTGCAA TGGCGTGATC TGGGCTCACT TCAACCTCCC	240
GTGCTCGAG	249

## (2) INFORMATION FOR SEQ ID NO:310:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTTGTTT NAAAAAAAAA AAAAAAAAAA AGGGCNGGGG GGAAAAAAAA AAAAAAGAAC	60
TCCTGGAGAG GGAAATAGCA AATGTGTCTT GCCTTTTGT TCTCTCTCTC TCTTTTTTTT	120
TCTCTCGTCT TCTTCTTTC TCTTCTCTC TCTGTTTTA AGTCAAGCAT TGGTCTCGAG	180

## (2) INFORMATION FOR SEQ ID NO:311:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

NNNNNNNNNN NNNNNNNNNN NNNNNNNANN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	60
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	120
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	180
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	240

```

NNNNNNNNNA NNNNNNNNAN NNNNNNANNN NNNNNNANAN GNANNNNNNN NNNNNNNNNN 300
NNANANANNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNC CCCCTTTGTC 360
ATNGTTNTCG TTCCCNITCT TCCTTGTTTC TTTTTCGGCA CAATATTCA AGNTATACCA 420
AGCATACAAT CAACTCCAAG NTGGGAATTT TAATTACTTC ATGGCCTACT TGATGCAGGC 480
TGGAAATGTTA TCCCTGGGGT GTGCTTGAC CCCACCTGCT TTCTTTCTCT CCTGCCCTC 540
CCCTACTCTC ACTGTAATT ATGGACCCTG CCCGCCTGCG TGTGTGTGT ATGTCCTGTG 600
CCTTTTCTCA CTATTGTTG GGTGTGGGAG GGGGTGGTTT TTCCTGAAA AGGGGGGTAC 660
ACCTATAGCT TTCTTGATGT TCAATCAATC AGTCACTGTG TCCAGACAT ATTCAATAAA 720
CACAGATTGG TACCATCTCG AG 742

```

## (2) INFORMATION FOR SEQ ID NO:312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

GCGATTGAAT TCTAGACCCG CCCAGGAGC CTCCAGCTGC CTAACCAGTG CCATTCTTTC 60
ACAACACGAT TTTCTACAAA TCTACAGCAC AACCGAGTTT GTAACCCGTG GGTAGTATG 120
AGGACCGGGT TCGGTACTC TCTGTATCTC CTCTTAAGCT TCGTCCAGGG TTCTTTATT 180
TTGTCTGCTG CCAATGTGCT CTCGCATGCC TGCACCCTCG CATGCACGCT GCCCGCATGC 240
CACGTGCCAC GCTGTAGCCA CATCCTCGAG 270

```

## (2) INFORMATION FOR SEQ ID NO:313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

GAATTCGGCC TTCATGGCCT AGTTGATGTC CTCTCATATT TTGTTGTTTA AATACGCAGT 60
GTGGTGGTTG TTATTAGGA CTGCCTCTGC TCTGACAGAT GTGTCTACTC TACAGAGAGA 120
GAGAGAGACT GTGTCTATTG TCCCACCAGG CTGTCCAGAT CCAAACCTCCA ATGACCTTTC 180
TGCACCTCTG CTGGCTATTG GTTACAGTTT ACATTCTACC TTCTCCCAAG GTATTGAGGG 240
AGGCTTGCAT GCAATTCTCG AG 262

```

## (2) INFORMATION FOR SEQ ID NO:314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

GAATTCTAGA CCTGCCTCTC CTGACACGGG CCACCAAACC CCTTACCTGG TTCCTTGCTG 60

```

TAAAACTTCA CCAAATGAAG CCAGAGTTGA TCATGACCCT CTCGTGCTCG AATCCCTTCT	120
GGGCTCCCCT CTGCCCCCTG CAAAGCCAC ATGATACCAC AGAGAAGACC TGTCCCCTGC	180
AGGCCAGCTG CTTAGCCTC TCCCTCACA CACATCGTCC CGCACACGGC AGCCACCATG	240
GACTCAACAT CCCCACACA CGGTGCTGCC CTCTGCATGC ACCGACCCCG TGCCCTCCC	300
ACCAGCTCGA G	311

## (2) INFORMATION FOR SEQ ID NO:315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCGGCC TTCATGGCCT ACCTAGGTGC TTTTAAAT ATTCAGACAA ATATCTATCT	60
TACATTGATT AAACCCGTGT AAATTCATTT GCAGTATCTA CATCGAATGT CAAAAAGTA	120
TACTTATTT TGTTCATAC TTATGTACAA TTTTCCCT CTTCAGGCTT TTTCAATTAC	180
CTTTTGAAG AAGCACTTAC TCTCCCTTC CCTATCACC CATCCCTCG AG	232

## (2) INFORMATION FOR SEQ ID NO:316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTCGGCC TTCATGGCCT ACAGTTGTTT ATACTTCCTT TACAAATATA AAGATAGCTG	60
TTTAGGATAT TTTGTTACAT TTTGTAAAT TTTGAAATG CTAGTAATGT GTTTTACCA	120
GCAAGTATT GTTGCAAACT TAATGTCATT TTCCTTAA GA TGGTTACAGC TATGTAACT	180
GTATTATTCT GGACGGACAC TCGAG	205

## (2) INFORMATION FOR SEQ ID NO:317:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAATTCGGCC TTCATGGCCT AGGGCTTGTC TTTTCATTG TTGAGTTGCA GGAGTTCTTT	60
ACATATTCTG GATACTAGAC CCTCATCAGA TATGGTTTTA AAATACTTTC TCTATTCTT	120
TTCATTTTCA AGTATCCCTT TGATGCACAC ACCCAAAAAA GCAAAATAGTG TCCAATTGCA	180
TTCTTTGATG AAGAAGAATA CAAGCAGTAA GTCAATTACA GCCTATTTT TCTTTTCTT	240
TCTTTCTCT TCTCTCTC TCTTTCTTC TTTGAGGCAG GTAGGCCATG AAGGCCGAA	299

## (2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 95 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```
GAATTCTAGA CCTGCCTCGA GCTCCAGCTG CCAACACCCT TGGACACAAT ATTCCAGTCT    60
CCACTGCCCA TCTCATGTGG TTCAGGTTCC TCGAG                                95
```

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 109 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
GATGCTTGGC TCACTCCCG CTACTGGCCC CCAGACTTTT CCACCCAGG AAATGTCTCC    60
CCTGCCTGCA GCTTCAGCGA AAGCCAGGA GGCAGGCCAA TCACTTGAG              109
```

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 253 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
GAATTCGGCC TTCATGGCCT ACACATTCT GTACCTGGAA AAAAAATGTA TCTTATTTT    60
GATAATGGCT CTTAAATCTT TAAACACACA CACAAAATCG TTCTTTACTT TCATTTTGAT   120
TCTTTAAAT CTGTCTAGTT GTAAGTCTAA TATGATGCAT TTAAAGATGG AGTCCCTCCC   180
TCCTACTTCC CTCACTCCCT TTCTCCTTGG CTTATTTTTC CTACCTTCCC TTCCTCTGT    240
CTCCCCACTC GAG                                                         253
```

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 334 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GAATTCGGCC TTCATGGCCT AGGTTGTAAG TGATTTTATT TTTTCTTTTC TATTTTCCAG	60
TGTTTCTGTA ATGCTTTCAT ATTTCTTTTG GTAGTTAGAA AATAAAGGCT AATTTTAA	120
AAGAATATCA TAGTCTAAAA AATTAAAGGA TGCATAGAGT TCCCTCTTGA CTATGTGACA	180
TCTAACTGA ATGAACTGTC TCGTGGCAC AGTGAACAG CGCAGTCTCA GGATTCTGAC	240
AGATTTTGG ATCCCAGCTC TACCACTAAC CTTGGGCAGG ATTTTAGTCC CTCTGAGACC	300
TGCTTTCTCG ATTGAATTCT AGACCTGCCT CGAG	334

## (2) INFORMATION FOR SEQ ID NO:322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GAATTCGGCC TTCACCTAAA TACTCCTCCT TTTGTATCAT TCAGCCTTTT GTTTTAGTTT	60
GGTAAGTTT AAGAAATTC AGCAGCAAAG TTGTTATTCA GTGGGCACGA TGGACTCCAA	120
ATGCCTCAAG TTATGTATAC CTGTGGAGGT CACGTACTTC CAAATGTTC TCTTCCTCAT	180
CTTCTCCCTT TACCTGCACG CCCAGGTGCG CCAGCCGGGC CTCGAG	226

## (2) INFORMATION FOR SEQ ID NO:323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GAATTAAAT AAACAAAAGG CAGCCAAGGA TGAAAGGATT TAGTTCTAAG ATGTTTCACA	60
GTTGTGATT GTTTATTTTA ATCCTTAGTA GTAAATTAGT ACTAGAAGGA TCAGGTATAT	120
CTTCCTTAAT TCTTCCAGG GGAGAGAAAG TCCCATTTCT CGAG	164

## (2) INFORMATION FOR SEQ ID NO:324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324.

GAATTCGGCC TTCATGGCCT AAGCCTATGT TGATCTTGAA CTCCTGGGCT CAANCCNTCC	60
TCCTGTCTCG GCCTCCCAA TTGCTGGAAT TATAAGCACA TTACACAGTG CCCAGTCTAC	120
CTACATTTTG ACAGACATAT AATATTCCAT GGCATGGTTA CATTATTTCAG TTAAGAATGT	180
TCCCGGTTTT CTCTAAGATA ATGCTGCCCA TCTGTGTCTC ACTCTGGACA TGTAAGTAC	240
CTGCAAAGAC TTGGACTGCT TGAGCAGAGG GCCTGCTTTT GTTTTTTGT CTTCCTGCCT	300
GTTGTAACTT GATGCTGCCA AATGATCCTC TTAAATGATT GTACCACCT CCCTGCCACC	360
ACCAGATTTT AAGGATTCTC TGTACCTCCC AACACATGAT GACATCATAC ATGAAAAGTT	420



TTGCCTGCCT GATGGAATAA TTGAGTCAAG AAATAGGATG CTAATGGCAT CTTGCTTAC	480
CCGGTCTCCT CGAG	494

## (2) INFORMATION FOR SEQ ID NO:325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GAATTCGGCC TTCATGGCCT AGTTGGGTGT TGAGCTTGAA CGCTTCTTA ATTGGTGGCT	60
GCTTTTAGGC CTAATATGGG TGTTAAATTT TTTACTCTCT CTACAAGGTT TTTTCCTAGT	120
GTCCAAAGAG CTGTTCTCTT TTGGACTAAC AGTTGTCCTG ATGAATAATT TCAITTTCTT	180
CAAGTTTATG ACACTCGGAA CGTCAAGAAC TGGAGGTTTG TGCAATTTGA GACCGGTCGG	240
CACTGTGCAG AGATCAGAGT ACTAAGAGAC AGAGATTAAA ATGGCTATCC TCGAG	295

## (2) INFORMATION FOR SEQ ID NO:326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GAATTCGGCC TTCATGGCCT ACAAGGATAG AATTCATTCC ACCTATATGT ACTTAGCAGG	60
GAGTATTGGT TTAACAGCTT TGTCTGCCAT AGCAATCAGC AGAACGCCTG TTCTCATGAA	120
CTTCATGATG AGAGGCTCTT GGGTGACAAT TGGTGTGACC TTTGCAGCCA TGGTTGGAGC	180
TGGAATGCTG GTACGATCAA TACCATATGA CCAGAGCCCA GGCCCAAAGC ATCTTGCTTG	240
GTTGCTACAT TCTGGTGTGA TGGGTGCAGT GGTGGCTCCT CTGACAAATAT TAGGGGGTCC	300
TCTTCTCATC AGAGCTGCAT GGTACACAGC TGGCATTGTG GGAGGCCTCT CCACTGTGGC	360
CATGTGTGCG CCCAGTGAAA AGTTTCTGAA CATGGGTGCA CCCAGGGAG TGCTCGAG	418

## (2) INFORMATION FOR SEQ ID NO:327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC TTCATGGCCT ACAGACATCT AATCGGAATC TTGCTCTTGT TGCCAGGCT	60
GGAGTGTAAT GGCACAATCT CGGCTTACTG CAACCTCTGC CTCTGGATT CAAGTGATTC	120
TCCTGCCTCA GCCTCCCAAG TANCTGGGAT TACAGCCCTG AAAACCACTC GCTTGCAGAG	180
CGCTGATCA GCAATGCCTA CTAGTTCTTC ATTCAAACAC CGGATTAAAG AGCAGGAAGA	240
CTACATCCGA GATTGGACTG CTCATCGAGA AGAGATAGCC AGGATCAGCC AAGATCTTGC	300
TCTCATTGCT CGGGAGATCA ACGATGTAGC AGGAGAGATA GATTCACTGA CTTTCATCAG	360

CACTGCCCCT	AGTACCACAG	TAAGCACTGC	TGCCACCACC	CCTGGCTCTG	CCATAGACAC	420
TAGAGAAGAG	TTGGTTGATC	GTGTTTITGA	TGAAAGCTCA	ACTTCCAAAA	GATTCCTCCA	480
TTAGTTCATT	CCAAAACACC	AGAAGGAAAC	AACGGTCGAT	CTGGTGATCC	AAGACCTCAA	540
GCAGCAGAGC	CTCCCGATCA	CTTAACAATT	ACAATGCGGG	AACTCGAG		588

## (2) INFORMATION FOR SEQ ID NO:328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC	TTCATGGCCT	ACGACTGGGG	GAAATGTCTA	TTCTCCTGTG	TATCTCTGGG	60
CTTTTCTTGT	TTTTGGCTGC	CTCCTGCTCA	GTTCCCTCTCT	TTAGGTATTT	AGTAAAGCGT	120
TCATGTAATG	TCATTCTCGA	GGACCCAAAG	TGATGCTCTT	TAACATGGTG	AACAATGGTC	180
ACTATATGTT	GGGCAAAACAG	TTCTGAGGGG	CTACGCTGAG	ACTGAGCTGA	TTGTATGTGC	240
TGGAAAATGG	AACGAACTC	CTGTTCTTTT	TTGTTGCTAT	GGACTAGATC	TCGGCAAAGC	300
TTGCGTTCCT	GAGCCAATAA	GCCACTGGGT	CGTGCGAGGT	CCTCATCAAA	AGAGTCCATC	360
CGGACATTGA	CCTGTGCCTC	TCGAG				385

## (2) INFORMATION FOR SEQ ID NO:329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC	TTCATGGCCT	AGCAGTTCAC	CACTGCAAAA	CCACGGGGCT	GGGTGGAGGT	60
ATTCATGGGA	CACCGAGTGG	TATCACTAGC	AGCGGACTCT	GCATGCTTAC	TTAGAGCATA	120
AAAGGATAGC	ACCCTTGGCC	ATTGCCTGAC	ATGAACTCAG	TTTGAAATT	GCAGAGGTGT	180
GGAGAGCCAT	GGATGGGTTT	TATAATTTAT	TCTAATGTAA	TCTCTGTGCT	AAAGGCTGTT	240
TGAAAAAAT	AATGAAGTTG	ATGTTGCTTA	AGTTATATGC	AAATGTAAAC	TGGTCTTCCT	300
TCAAGATGTT	TGGAATGGAA	TGAATGCCCT	TCCCCTGGGT	ACCTCCCAAT	ACCTACCCTC	360
AAAAGAGCTC	CAGTAAGGCT	TCCTTATCTT	TCCTTGCCCT	GCTTCCTACA	CTGCTGCTGC	420
AGGTGTCTCT	GGGTGATTGT	GGGGGAAACC	ACTGTGGTTA	AGCACCAACA	CCAAGACTCG	480
AG						482

## (2) INFORMATION FOR SEQ ID NO:330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

GAATTCGGCC TTCATGGCCT AAGGCCTTGG TGCCCTGTGG GTGGACTCTG GGGAGGCCAG      60
GGGCCCCAAGG CCACCTTCTA GGGCCTGAGG AGCCCTCTGA GACCTGCACA CCCACCCAG      120
GGAGCGCCCC TCCCTCCACC TCTGTGCCCC CCCAGTGACT CTCGAACCTC TGTCTGTTTT      180
GCAGATTCAT CCGGAAGGGC CGCCAGCCAG TGGATTTCCT GGGCCCTCAG CCCTCTGGAG      240
TGTACGAGTT TTGGAGAAAC CTCTTCCTCT GTATATGCTT TTGACTTTCC TGGACTGATG      300
TAAAAATACT CTTTCTTTTG ACCTGTTTAT TTTTAAGACA CGACGTGATT GTGTCAGCTT      360
ATATTTTATT GCTGAAGTAA ATTTTCAAAT GTTTTATTAG TTTTITTTGA TCTTTGTCTG      420
CTCATTTTGG AGTTTTTGTA ATTTTGATAG GTGTTCTTTT ATGCTTTGTA TTGTTTTCTT      480
AATGACTTTT ACCTTAGTTT TTAACAAACC CATAGTACAG TGTACCCTCG AG              532

```

## (2) INFORMATION FOR SEQ ID NO:331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

GAATTCGGCC TTCATGGCCT ACATTTTGGG AAAAAAAAAA ATCTACTTTG TGTATGTGTG      60
GGGTGTGGGG TGTGAGAGAT ACATTCTTTT TTNGTGTCTA AATCTCACAG TCCACATATG      120
ACTTCCCCCA CTTGAGAAAT CTCTCTCATC TGTGTGGCTC CTGCAATTCT ATAAAAATAT      180
AAATAAATAA AATTTTAAAA AGTATAAAGC CGGTGCCATG AGACCCTTGG GTTGGGGCAA      240
GCCTGTGAAG TTTGAACCGG TTAACGCACG AATACAAGGG AGTGATTATT ACAAGGCCAT      300
CCCCTTAGC ATCGGGGAAT CATTGGGGA GAGAGATTCA ATTTCATAAA GATGATTTTC      360
AAGGGCTGTC TCGAG              375

```

## (2) INFORMATION FOR SEQ ID NO:332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

GAATTCGGCC TTCATGGCCT ACACGCGGTC AACTCTGCAG GGCTGATGAT AAACATGCCT      60
CTTCTCCTAT TGTCCITCTC CTCTCTAAAG CAAGGTCAAT TCTGTGCTCG TCAGGCAGTG      120
GCAGGGGTTG GGAGGAGGAG AGAGGGAAAC ACTGTGGTCA GGCTCTGGGG AGAGTTGACT      180
ACAGTGTAGC TCTTGGATTA TTTATGAATA TTGCCCTCAG ATTTATTTTC ACTCTGCTCC      240
TTCCATTTCAT ATTCCCAGAG ACAACCAAGA GCCGACTGTA GAAAAAGACT TCCAGACACC      300
TAGAATATAT ATCAATAGAC ACTGTTTAAA AGGGGAGACT CGAG              344

```

## (2) INFORMATION FOR SEQ ID NO:333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

TGGCCTAAAG	GGGGTGGGTA	CTCCGGTGGG	GTAAGGTCAG	AAGGTCCCTG	TGCAGGGAGG	60
GACTGGTCCC	TTGAGAAGGA	ACAGAGGGCA	AATCCTGAAG	AGTCCTGGAG	GCCCAATGTA	120
GACAGCAGAA	GCTGGGAGCT	GACCTAGGAG	TGATCGGGGG	CCTGATCCAG	ACAGGACAGA	180
CACAGGCTGA	CACCGGAGAG	TCCCAGGTGC	CAACATGAAC	AGTTAAGGCA	GGGGCTGACC	240
CCAAAGAAAT	CAGGGGCCCG	CAGCTGACCC	CGGAGGGTCC	CAGGTGCCGA	CCTAGACAGC	300
AAAGGCAGGG	CTGACCCAG	AGGGTCCCGA	GCCGACCCAG	ACGACACAGG	CAGGGCTGAT	360
CCCGGAGGGC	CCCGCCCCGA	CCCGGACAGG	CAGTGAAGGC	ACAGGCAGGG	CTGACACTCG	420
AG						422

## (2) INFORMATION FOR SEQ ID NO:334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GGGAACGAAA	GATGGCGGCG	GAAACGCTGC	TGTCCAGTTT	GTTAGGACTG	CTGCTTCTGG	60
GACTCCTGTT	ACCCGCAAGT	CTGACCGGCG	GTGTCGGGAG	CCTGAACCTG	GAGGAGCTGA	120
GTGAGATGCG	TTATGGGATC	GAGATCCTGC	CGTTGCCTGT	CATGGGAGGG	CAGAGCCAAT	180
CTTCGGACGT	GGTGATTGTC	TCCTCTAAGT	ACAAACAGCG	CTATGAGTGT	CGCCTGCCAG	240
CTGGAGCTAT	TCACTTCCAG	CGTGAAAGGG	AGGAGGAAAC	ACCTGCTTAC	CAAGGCGCTG	300
GGATCCCTGA	GTTGTTGAGC	CACCTCGAG				329

## (2) INFORMATION FOR SEQ ID NO:335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC	TTCATGGCCT	AAAACAGATA	ACGCTATAGA	GAAAACACTG	TTTACTGAAC	60
AGTGCTTTGA	AACCACGAGG	GTGATCAGAG	CCCCATTTCG	CCTTCTAGAG	ATAAACCTGT	120
CTCCCTTCCT	GCAGAGCTAG	CTCCTCCTAT	TGCTTCTGGT	TGTCGTTTGT	CTTCAGTCTG	180
CTTCCTGCCA	GTGCAGCAGC	TCCTGCTAGA	TCTTGACATC	CTAGTGGCCA	GATCCCAGGG	240
GCGGTGCTGG	TCCTATCCGA	GCTCTCTGCC	TCATCTCCCA	TTCTTTTITT	CCACACTCAG	300
TGTGTATTCT	CTTGATTTC	CATACCCTGT	TCCTCTACC	ATCCACCTCT	CTACCTCATC	360
TCCCGACCTG	CCTCGAG					377

## (2) INFORMATION FOR SEQ ID NO:336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```

GAATTCGGCC TTCATGGCCT AGCAGGTCAG GAGCCCGGGG AAGGCCCAGA GGTACTCCAA      60
AGGGGGCCCG CTGGTATCTG AAGGCCCCCTT GCAGTTAGTG TGTGTTGAG CTGTGGGCAT      120
GAACATGCCA CAGGCAGACA CTGTTTAGCC AGGGTTTTAA GAAACACGGA GGGTCCTGTG      180
GATCTGGAGT TCATTTGTCA GGACAGGGAT GGGGACCCCT CTGAAGTATT CACTGTGGGC      240
TGAGGGGTGC TGGCCACACA ACCTCTGTGG GAGGCATCTC TTGCAGTGAA GCTGTTGGTC      300
CTCAGTTCAG TGCCCACTGA GGGTAACCAG GCCCCAGCTC TGCACCCCA CTCGAG      356

```

## (2) INFORMATION FOR SEQ ID NO:337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

GAATCTAGA CCTGCCGAG CACAATCCCG TGGACAGAGC TTAATCCATC TAACTCGTTT      60
TCAAGTGCAT GATTITCACT TTCACTTTTC CTTTTCCTT ATTATGTTGC TTAACITGTA      120
CAGTGGCAAC TGAAATGCAT TTCAGAAATA GGAGGTTTCG TCCAGCACCC TCTGCAGCCT      180
TGGTGCTGT AGCTCTGGAC TTCCCTGGGC CTTTCCCTGT GGGAGGGCCC TGTAGACCAC      240
ATCAGGGTGG GGTGGGGGTC ACTTGGCAAA AAGGGCCGAG GTCTGGTGAT GTGGTTCCCA      300
GGATCTGGAA CCTCTCCAC CCCTCCTGCA GTTGGACTGA ATTCTTCCCT TTCATCCGAA      360
GAAACCCACT TGCTGTTTCC AGCCAACTCG AG      392

```

## (2) INFORMATION FOR SEQ ID NO:338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

GCAAGATGGC GACCGAGACG GTGGAGCTCC ATAAGCTAAA GCTTGCCGAA CTAAAGCAAG      60
AATGTCTTGC TCGTGGTTTG GAGACCAAGG GAATAAGCA AGATCTTATC CACAGACTCC      120
AGGCATATCT TGAAGAACAT GCTGAAGAGG AGGCAAATGA AGAAGATGTA CTGGGAGATG      180
AAACAGAGGA AGAAGAAACA AAGCCCATTG AGCTCCCTGT CAAAGAGGAA GAACCCCTG      240
AAAAAACTGT TGATGTGGCT CTCGAG      266

```

## (2) INFORMATION FOR SEQ ID NO:339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

GAATTCGGCC TTCATGGCCT AAACAATGAA TAAAGCCAAG CCAGTTCCTG CCCCCTGGA      60

```

GCTTGTAGTC	AAGACATTGA	ACAAGTGATC	AGAAAGATGT	TGACTGCTGC	AGCAGAGGGT	120
TGCAAGCTGC	TCATGAGTAT	ATAACAAGTA	GCCCTAACCA	AAGCATTCTC	TCCCTTGGTT	180
TAATGTCCAC	CCATTGAGGT	GACTGCTAAA	TACTAATCCA	TGACTCTATC	CCTTGGCATT	240
CAAACTACA	CATCCACTTA	CCTGCCTCTC	CAACCTCCCT	GCCTCGAG		288

## (2) INFORMATION FOR SEQ ID NO:340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GAATTCGGCC	TTCATGGCCT	AGTCTCTGCC	ATGTTCTAAA	CTGAAAACCT	CCTAGTCAAC	60
TTCACACITT	ATTCCCTGAT	CCTCAATTGG	TCCCATGTC	CCGTTAGTGT	TTCTTGTAAG	120
CCTCTGCCAC	CACCGCAGAT	CGAACTCTAA	TCACATCTCA	CCTGAATTAT	GGAAAAGTCA	180
CCTCAATTCT	CTCACCCTATC	CCAGCCTCCA	CTATGGATTA	ATATGCCTAA	AGCAGAGCTG	240
ACCACAACGG	TGAGAAGAAT	CTGAGAGGGA	AGCAGCAGCA	AACACAAGAG	TCACTGGACA	300
TGCATGCCTC	GAG					313

## (2) INFORMATION FOR SEQ ID NO:341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCGGCC	TTCATGGCCT	AAGAAAAAAG	GATAGACAAA	TAGTATTTTT	GTGATTTTAC	60
AGTAGCTTAA	AACTATAGGA	TTTTTTTCC	CCATTACTTT	GCAACAACCTG	ATACTTTTGA	120
CCAGTTCTCT	TTCTAAGCA	TTTCTCTCT	TGAGCTATTA	CCCAAATTGT	CCTAGTTCTT	180
CTCTGCTTGT	CCCTCAGCTA	TACACAGTCA	CTGAGGCTCT	GTGCTTGGCT	TCTGTTCTCT	240
TCTCCTCATA	GGGATTCCCT	ATGTTGGAGT	TCATCAAGCT	CGAG		284

## (2) INFORMATION FOR SEQ ID NO:342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC	TTCATGGCCT	ACCACGATAG	ACCAGCTGTA	GCTCATTCCA	GCCTGTACCT	60
TGGATGAGGG	GTAGCCTCCC	ACTGCATCCC	ATCCTGAATA	TCCTTTGCAA	CTCCCCAAGA	120
GTGCTTATTT	AAGTGTTAAT	ACTTTTAAGA	GAAGTGGGAC	GATTAATTGT	GGATCTCCCC	180
CTGCCCATTG	CCTGCTTGAG	GGGCACCACT	ACTCCAGCCC	AGAAGGAAAG	GGGGGCAGCT	240
CAGTGGCCCC	AAGAGGGAGC	TGATATCATG	AGGATAACAT	TGGCGGGAGG	GGAGTTAACT	300

GGCAGGGCAC TCGAG

315

## (2) INFORMATION FOR SEQ ID NO:343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GAATTCGGCC	TTCATGGCCT	AAAGATGTTA	GATATTACAA	TTTGACTGAA	GAACAGAAGG	60
CGATCAAGGC	CAAGTATCCG	CCAGTCAATA	GGAAGTACGA	GTGTGAGAGA	TGACTTACAG	120
TCTCTTCTGT	TTCACTTTTT	GGATGAATGG	CTTTATAAGT	TCAGTGCTGA	TGAATTCCTC	180
ATACCCCGGG	TGGGGAGAAG	AATTTTCATT	GTCCAAGCAC	CCTCAGGGAA	CAGAAGTCAA	240
AGCAATAACA	TATTCAGCAA	TGCAGGTCTA	TAATGAAGAG	AACCCG		286

## (2) INFORMATION FOR SEQ ID NO:344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GAATTCGGCC	TTCATGGCCT	ACCTCTGTGA	AAATTTAATT	TTTTATATCC	TGATTAATAT	60
ATGTGACTT	TAGGCCCAT	TTTCATGTGC	TTCACTTTGA	TAGAGTTAAT	CCATAAAATT	120
GCTCTTTACT	TTAGCTTATC	AAATGAAGTA	TTATTTGTG	GA CTGGAGGC	CAAAAAGTCA	180
ATGTGAGCTT	CTCACAGGTT	TTTAAAGCTC	CATAAAAAT	AATTATCCAC	TTGTCTTTAC	240
TTTGTGTGAC	CAGAATAGTT	GGTAACTCTG	CCAGAGCCTG	TACTTACCTG	CCAAAAACAA	300
TTAAATCTGG	TTAATGCCTG	AAACCAAATC	TCTCAGTCTC	AAGTGTATA	CTATCCAAGT	360
TTTAAATGGA	AAGGTAAACT	GTGGAGTAAT	GAAATTTTGG	TTTTACTGTA	CCTTTTGCTA	420
TCAAGATAAT	ATTTCATGTT	GAAATCTTGT	CTTTATTTGG	AATTTAGTTA	CTGTCTGCTT	480
TTAACCTTTG	CTTTCCTAAA	GAAAGTTTGA	GATCCAGAGA	GTTCAAGGGA	TCGGGGAGTC	540
TCGAG						545

## (2) INFORMATION FOR SEQ ID NO:345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GAATTCGGCC	TTCATGGCCT	ACAATAAGTG	TGTTATACTT	GCTTTGGTGA	TTGCAATCAG	60
CATGGGATT	GGCCATTTCT	ATGGCACAAT	TCAGATTCAG	AAGCGTCAAC	AGTTAGTCAG	120
AAAGATACAT	GAAGATGAAT	TGAATGATAT	GAAGGATTAT	CTTTCCAGT	GTCAACAGGA	180
ACAAGAATCT	TTTATAGATT	ATAAGTCATT	GAAAGAAAAT	CTTGCAAGGT	GTTGGACACT	240

TACTGAAGCA GAGAAGATGT CCTTTGAAAC TCAGAAAACG AACCTTGCTA CAGAACTCGA 300  
G 301

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCGGCC TTCATGGCCT ACACATTTTG ACAGCTTCCT TTCAGGTTTC TTGAGCTCTC 60  
 AGAAAAATTA GAAGGAAGTG GGCTGGGGAT ATAGAGAGAG TCCAAACTAC CAACTAATGA 120  
 ATGAATCTGA AGGAGACACA GAAGGGCAAG TAGAGTTTAG AGTTTGAGAG TGCAGGAAAG 180  
 TTTTGAAATG GTCAGAACTG CCAGAGTAAT TTCTGAGATC TTAATAAGCA CTCTCCACC 240  
 GTTTGCCTTA AAGATACCCC TTCCCCCAA TTGAAACATC ACAAATCTGC AGAGCTCTTT 300  
 AATCAGGTGT GTTATACACA ATGAATTTAA TTCTCTTATT GCCCTGGAAG AAAGATAAAC 360  
 CAGATGTGGC CCTTGCCCTT TTTAGTAAG TATTTGTTAG ATCTTCATTA CATTTAGGC 420  
 CTCCTAGGCC ATGAAGGCCG GCCTTCA 447

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 297 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GAATTCGGCC TTCATGGCCT AAAATTCGGC TGATTTCCCC CTGGCTAGC CCAGCTGACG 60  
 GAGTCAAGAG CAAACCAAGA AAAACTACAG AAGTGACAGG AACAGGTCTT GGAAGGAACA 120  
 GAAAGAACT GTCTTCCTAT CCAAAGCAA TTTTACGCAG AAAAATGCTG TAATTTCTTG 180  
 GGAAGATTTT AATGTACACC TATTTGTAAA GTCATCAGAA TAGTGTGGAT TATTAAATAT 240  
 CTAGTTTGGA AGAAAATAAT TTATATAAAT TATTGTAAAT TTTTATGTAA ACTCGAG 297

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAATTCGGCC TTCATGGCCT AGAATAAAAC AAAGCCTTTT CTGCCTTTTA CATTAGTTC 60  
 AGTAACCGTC AACACCCAC CCATATACTC CCATACCATG AGGTGTAAT TTCAAATCC 120  
 TCGCATACTT TTAATTACTA GTTTAATTAT TTGCCTTCTC ACTGAGTCTA TAATCTCACT 180  
 TAGGGTAAGA ACAGAACTCA ATTACAGATG CTCAGTAAAC ACTGGAAGGC CGCGGCTCGA 240  
 G 241



## (2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```
GAATTCGGCC TTCATGGCCT AGGGCTGCCC AAGATTGTGA AAGGTAAGTA GTATCTTTAT    60
TTGGGGGTAA CTTAATTATA GATAAAAGAT GGTCCAATAC TGGAAACTGT TCGTTTCTTC    120
CCTTGGATCT AGTCTTCTTC TGCTTTATAT AGAATCCCAC CATCATCTCG AG            172
```

## (2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```
GAATTCGGCC TTCATGGCCT ACACGTGACA GCCTTTCCTT TTTCAGATCA CCTTCCTCAC    60
ACTGATGGTC TCATACAACA TCATTTTGAA TGTCTCAGC TCTCTGCACC ACCCACCCAA    120
CTCCACTCTG GGCCACCGCT GGTGTATCCA AGATCAGGAC ACCAGTCCCT GGGCACCAGG    180
GAGTATGCTG GCCACTGAAG CAGCTTCGTT TTTCCGGCAC CCATGTTGTA AAATCGACTC    240
CCCCAACTC GAG                    253
```

## (2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```
GAATTCGGCC TTCATGGCCT AGAAAGTTTA AAGATTAGCG TACTGATTAT GATGGGATTT    60
TTACTGAAAA TTAGTTTGT CAGGCTGCTT GCTTGTCTGT GTATTTTCTA TTCTAATTTA    120
GTTTTTATTT TTATCAAAGC TGTATTACT TATAATGTAA AAAGTCAATT AGTTTTCCAA    180
GGCTTATTAT GGAAACAGT AGTCCCCAG GCTCCCATCC CTATGTCCAA CAAACTCGAG    240
```

## (2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```
GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAAGCCTTT GATTATTCAG CTGCCACTGC      60
CTACAGGCCT TCTCCCATAT TCCTTCCTTC TTGCTAAGTC TGACTTAAAC TAGGCTTAGG      120
CACCAACTCC TATAGGAAGC CTTCTTGAA CTTGGCCCTC TACTTTTCAC TCACTGACTA      180
CCACTCAATT AACTGAACGG TGAAAAGTAA CCCACAGCTA CGCATTTCATG CAGACAACAG      240
AATTTTACTA CTTCTTCTCA CTACTGGTTC ATATTTCTGC AACCAGAAAA TATCATTTCA      300
TCCCTAGTAA CTATGGCTTC CATCTGTAC TTCC                                     334
```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```
GAATTCGGCC TTCATGGCCT AATAATGACT TGTGGTTGA TTGTAGATAT TGGGCTGTTA      60
ATTGTCAGTT CAGTAGGCCA TGAAGGCCGA AG                                     92
```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```
GAATTCAGTT CCTTATATAT TCTAGTTATT AATCCCTTAT CAGGTGGATA GTTTGCAGAT      60
ATCTTCTCCC ATTCTTTAGG TTGTCTCTTC ACTCTGTTGA TCGTTTCCTT TGCTCTGCAA      120
AAGCTTTGTA GCTTGAGATA ATCCCATTTG TCTGTTTTTG CTTTGTGTGC CTATGCTTTT      180
GAGGTCTTAC TCAAAAAATT TTTGCCCAGA CAGTACCCT TGAAGCATG CCCCATGGT      240
TTTTTTTTT AGTCATTCA TAGTTCAGGT CTTACTCGAG                               280
```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```
GAATTCGGCC TCCATGGCCT ACATAGATGG GCACACTCAC ACACAGAAGT GTGCTTGATC      60
AATCACCACA CAGCACAAA CACACACACA CACTAAAAAT ATAAACACA TCGCTCACAT      120
```

GGGCATTTC	AATGATCAGC	TCTGTATCTG	GTAAAGTCGG	TTGCTGGGAT	GCACCCTGCA	180
CTAGAGCTGA	AAGGAAATTG	GACCTCCATG	CAGCCCTGAC	AGGTTGTGGG	CCCGGGCCCT	240
CCCTTTGTGC	TTTGTATCTG	CAGCTCTTGC	GCCTTTTATA	AGTCCATCCT	AGTCCCTGCT	300
GGATGGCAGG	GGGCTGGATG	GGGGGCAGGA	CTAATACTGA	GTGATTGCAG	AGTGCTTTAT	360
GAATTCACCT	TATTTTATCG	AAACCCATTG	GACTCGAG			398

## (2) INFORMATION FOR SEQ ID NO:356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GTGTCAGAGC	AGGCATTTCC	CAACCTAAGG	AAATCTTTGT	TTTCAAATAT	TAGGGTTTTT	60
TTTTAATTGT	GGTTAAAGGA	TTTTGGACAT	GCTTTGTAAA	TTGTTAGTAA	AAGGACCTAT	120
TTTCCACCTG	TATTCTAAGT	TATTTTTTTC	CCTCTTTTGT	AATTTTTCAG	GTGAGCCCTT	180
CATAAACCCA	GATGGGAGTC	CAGTTGTGTA	TAATCCTCCT	ATGACTCAAC	AACCAGTTAG	240
ATCCCAAGTG	CCTGGACCTC	CACAGCCACC	TCTGCCAGCC	CCACCTCAAC	AACCAGCAGC	300
TAATCACATT	TTCTCACAGG	CGCATCTCGA	G			331

## (2) INFORMATION FOR SEQ ID NO:357:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GCTGCCTCGA	GGTCTCCAAG	ACTTTTTCAT	CTCGTATCGT	TTGCGGATCC	GTATCCATAC	60
TTTTATTTTC	ACTTTCCTCC	TCTTCCTCCT	CGAACTCCTC	GTGCGCATCC	TGTCGCCCCA	120
GCTTCCCGTA	GCCATCCTCG	CCTTCTTTCT	CGTGCTCCTT	CTCGCTCTCG	CCATCCCTCG	180
GCATACTCTC	CCTTTCCTC	TCGAG				205

## (2) INFORMATION FOR SEQ ID NO:358:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CAAAAGAGAT	GGTACCAGCA	AGAGATTAAT	ACTAAAGAAA	TGCAGTCAGA	TTTTAAAGAA	60
ACTGGAAGAA	GAGCCATTTC	TCCCAGGGAG	AAGATTCTAG	ATGTGATTGA	TGACACCATA	120
GAAATGGAGA	CAGGTCTGAA	AGCAATGGGA	AGAGAGATTT	GTCTAAGGGA	GAAGACGCCA	180
GAGGTGATTG	ATGCCACTGA	GGAAATAGAC	AAAGATTGG	AAGAAGCTGG	AAGAAGAGAA	240
ATATCCCCAC	AGAAAAATGG	CCCAGAGGAG	GTAAAGCCTC	TAGGTGAAGT	GGAGACAGAT	300

TTGAAAGCAA CTGGATATGA GAGTTCCCCA AGGGAGAAGA CACCAGAGGT GACTGATGCC	360
ACTGAGGAAA TAGACAAAAA TTTGGAAGAA ACTGGAAGAA GAAAAATATC CCCAAGGGAA	420
AATGGCCCAG AGGAGGTCAA GCCTGTAGAT GAAATGGAGA CAGATTGAA CGCAACTGGA	480
AGAGAGAGTT CTCCAAGGGA GAAGACACCA GAGGTGATTG ATGCTACTGA GGAAATAGAT	540
TTGGAAGAAA CTGAAAGAGA AGTATCCCCA CAGGAAACT CGAG	584

## (2) INFORMATION FOR SEQ ID NO:359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GAATTCGGCC TTCATGGCCT ATGCTTTCTG AATTGGCAAG ATATTCAGG CTTATTTGGC	60
ATTCATCTTA CTCTAGACCT ATTATCAACC ATGTCTCAA GGATAAGTAG ATCCGTTTAA	120
GGGAAAATGG TATTTTGAAA GCATAGTGTG GGATCTGAGG ATACCTATTC CTGTCAGGTT	180
GGTTATTGTT TGTTTTCAGT GAGTAGATCT TGGACTTTAT TAATTTTATT TATTTATTTT	240
AAGAAAAGTA CATCATGAGT TATAAGTAAT AATCCAAC TAAATTTTAA TATTGCTTAA	300
CTTCTTTGAT TTTATATTTA TCTTTTACAC TGAAAGTCT CGAG	344

## (2) INFORMATION FOR SEQ ID NO:360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GCGGGTGGAC AAAAATGAAG CCAATGAAGA AGGCATGCAC TGGCCTTTCA GGTCTGGCA	60
GTGGCAGCAA GTCCCCCCA GCCACCAGGG CCAAGGCTCT GAGGCGGCGA GGGGCTGGGG	120
AGGGTGACAA GCCAGAGGAG GAGGATGACG AGGCACAGCA GCCGCAACCA CAGTCGGGGC	180
CCGAAGAGGC TGAGGAAGGG GAGGAGGAGG AGGCTGAGCG GGGCCCTGGG GCTGAAGGTC	240
CTCCACTGGA GCTGCACCCT GGCAGCCCG CTCCAGGCC AGCAGAGGAC CCCAAAGGGG	300
ATGGGGAGGC AGGCGCTGG GAGCCCTCAC TCAGCCGCAA GACAGCCCCG TTCAGTCTCG	360
AG	362

## (2) INFORMATION FOR SEQ ID NO:361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GCACCACCTC TTGCACTGTG AGGAGTTTAT TGATGAATTC AATGGGCTGC ACATGTCCAA	60
GGACAAGAGG ATCAAGTCAG GGAAGCAGTC CAGTACCTCC AAGCTGCTGC GTGACAGTCG	120

```

AGGCCCGTCG GTTGAGAAAC TGTCCACAG ACCTTCAGAT CCTGGAAAGA GCAAGGGGAC      180
CTCCCATAAA CGGAAGCGAA TTAACCTCC CCTGGCCAAG CCAAAAAAAG GGTATTGAGG      240
CAAGCCCTCT TCAGGAGGTG ACAGGGCCAC CAAGACGGTG TCTTACAGGA CTACCCCCAG      300
TGGTTTGCAA ATAATGCCCC TGAAAAAGTC TCAGAACGGG ATGGAAAATG GGGACGCCGG      360
CTCTGTAAGG ACCTCGAG                                     378

```

## (2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

GATTGTATTG AAAGTCAGAC ATAGGTGTGG AACCAGTTAT GGGAGTGAGG ATAAGTCTAG      60
ATTTGGGAAT CAGTCGAGAC GAGGTGGACG ATGAAAGTCT GAGAAGAAAG GATCTTGCTA      120
ATGGAGTGAA CTCAGAGCTT GATAAAGGGA GGATGAGTGG AAATGGAGCT CAACGCTGTG      180
CCTTGGGAAA TACCTCTGTG GATTGGTGGG AGCACAGTGA GAAATTCAAG AAAGACACAG      240
ACAATGGAAT AACCAGAGAA CTCGAG                                     266

```

## (2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

GAATTCTAGA CCTGCCTCGA GCATTGCCCC CGGCCTAAGA AGCTCTCTTA TCTTGCATCT      60
TGGGCTGGAC TCCTACAACA GCCCAACTT CCGTGCTGGT CTCCCAGCTT CTAGCCTTCC      120
CCCATCTCCT GTCGTTTTCG ACACAGCAGC CAGAAGGATC CTTTAAAAAC AGAGGTTGAT      180
CCTGTCGTTT CTCAAAATCC TCCAATGCTT TTCCTACTGC ACTCAGAGTA AAAGCCAGTC      240
TCTGCCTTAG ATGCTCTGGG ATCCTGTACC CTCITTGGTC TCATGTCCTA CAATCTGCAT      300
TCTGGCCATA ATGGTCTTCT CTGCTGTTCC TTGAACATTC CAGGAACATT CCCCCATAC      360
CCTCGAG                                     367

```

## (2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

GAATTGGGCC TTCATGGCCT ACTGGGTTCT GAGAAGCAGT GGCCCGAGCT GAAGCATCCA      60
GACAATGAGT GTTCAGAAGC TGCCAGATTC TCACCTAGCC TTAGAAGTAA CACAGCCACA      120
TTCTGTGGGT TACAAACACA TTTCTAAGGC CAGTCCAGAT TCAAACGGAG GGCAATTAGA      180

```

TTTGACCCCT TGATGAAGGA GGGCAAGGTT ACACTGAAAA ACAGCATAGG GACTGGGAGA	240
TATTATGATG TCCATTTTGG GAAAATCTGC CACAGACACA GTGAAGACAG AGAGCCCTTC	300
TCTCTGATCG AGGACCTCCA GAATGATCTG CTGAGTCACT CAGGTATGCT GGACCATTCA	360
CACTCACCCC GAAAAGCTC GAG	383

## (2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GAGGTTTACA GGTTTAAGCA TTTGTTTTTA CAAAAGGAA TGGGATATGG GGGTGGTCAA	60
GTTTTACGGG TAATAACAAC ATTCTCTCTA GATGGCAGGG GGTAAGTCTG CCTGTCCTCC	120
ATTGCTGGTA CCACATAAGG GATACATTAG TAAAGTAGGG AAAGGGTCAT ATGTGTGGTT	180
GACCTGTTCT TCAGAGAGGA ACGTGGGATG GTATCTGCTG TGTACCTGTC TCAGACCAAA	240
CCTGGGGGTG GACCAAGTGC CCTTTCTTCT CAGCCTTCTT CCACAGCCTG ACTGTACTGC	300
CACCCGCACC CATGAGAAGG AGGTNNTGAA GGAAGCTTGA GGACATCCAC CTCGAG	356

## (2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GAATTCGGCC TTCATGGCCT ACAACCATTG AAAAAATATA GACTTAGAAA ACGAAAGTTC	60
CCCTTAATCA CAAAGAACCA CAGTTGACAG GGTGATAGA TGTTTTTTCA GATTTTTTTT	120
TTCATATGTC TGCTATCTTT CCCCACAGGA ACTGGGTTTT ATTTTAGGTG TTGTTTTGCA	180
ACCTCTGTTT TTCAGTTGCC AGTTTATCTC AGACATTGTC CTATGTCAGT ACAGGCCCAT	240
CTCGAG	246

## (2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GAATTCGGCC TTCATGGCCT ACAAAAAAAC AACTTTCCAG TGGCTTCTCA CTGCTCTGAG	60
AATAAATCC AGGCTCTTCC ATTGCAACCA ACAGGATCTG GTGATTGAC CCCAGCCCCT	120
CTTTCCAGGC CCTCATCACC TTGATCCTCC CTTAACCTAT CCTGCTCCAG CTGCACTGGC	180
TGCCTTCCTA TTCCTCCAGC ATACCAAGAT TGTTTCTGCC ACAGGGCCGC CACTCGAG	238

## (2) INFORMATION FOR SEQ ID NO:368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```

GAATTCGGCC TTCATGGCCT AGTTTTTCT ACTCCTACAA GTGTAAATTG AAAAATCTTT      60
ATATTAAAAA AGTAACTGT TATGAAGCTG CTATGTACTA ATAATACTTT GCTTGCCAAA      120
GTGTTTGGGT TTTGTTGTG TTTGTTGTT TGTTTGTTT TGGTTCATGA ACAACAGTGT      180
CTAGAAACCC ATTTTGAAAG TGGAAATTA TTAAGTCACC TATCACTCGA G                231

```

## (2) INFORMATION FOR SEQ ID NO:369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```

GAATTCGGCC TTCATGGCCT ACTTGGTCTT CTGCACTTTT GTCTCTGACG TACTTCCTTT      60
CTTCACAAGT GCCATTACA GAAAGCTGGG CTTAAACCAT TCCCAGCTAT TCCTCCTACA      120
GCTTTCCTGA ATTATTCAG AATACAAAAT TCTGTATCTC CAAGAACTA TTACAGATTT      180
AGATTTAAAA ATATGCACTA TTTTCTACCT TGTATGTTTT GCTTACTATT TTTTITTTGC      240
AGAGGATATG TCTTAAAAAT TGAAATGCAT CAAAAAT                277

```

## (2) INFORMATION FOR SEQ ID NO:370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

GAATTCGGCC TTCATGGCCT ACCAAGTCAA AAAATAGAAC AGTTCGGCA CCCCAGAAGC      60
CCTTTGCCAC GTGGTCACAA CCTCCCTGT TTCCACCAAC AGTAACATTC TAGTTTTTAC      120
AGTAATTCT TCCTTGCTTT TCTTTGTAAT TTTACTGCCC TGTGTTTCTT AATATGATTT      180
AGTTTGCCT GGTTTGCCT TCATATAAAT GAAATCATAC TGAATATATT ATTTTCATATT      240
TTGCCCAATA TTTTGTGTGT AAGATTCATC CATCTTGTAG CTCCAATGTA TTTATTTTCA      300
TTTTGTATA ATTATATGAT TATGCCACAG TTTGTCAGTT CACTCGAG                348

```

## (2) INFORMATION FOR SEQ ID NO:371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GAATTCGGCC TTCATGGCCT AGAATTATTA GGAAACAAAT GGTTTTGCTG TCTTTTGCTC	60
ATTAGCTTGG CCCCATGTTT AAGCATTTCG TAACAACTGT GAAGAGCCTG CTACAAATAA	120
AGTGCTAGGT GCTCTGAAGA AAAATAAAGC TGTTAAAGGG AATAGAAAGT GATGAAGGCA	180
GGGGCTGTTA GACAGGCTGG TCAGTGTCTG AGGAAGTAGC CCTGCACTGA GACCTGAAAA	240
GTAAAGAAGC AAGCCATGGG GAGTTGGGGA GGAGCATTCC AGACAGAGGC TTGATGTGTT	300
GAACCATCTT TTCCAAGCTC TTCCTCTGTT ACCTTCTCTT TAGTCACTAT GTCCCTTTTC	360
TATCCAGAC CATAATTCCA CCATTTATCT TAAGGCTGAG	400

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GAACGATTGA ATTCTAGACC TGCCTCGAGA TCAGCACTAA CCCCCCAAC TCCCAGCCTT	60
TAGTTTGCTG TAGGCTGTCA AACAGATAA CCAAACTTGT TAAATTGAGA ATCAATAGGC	120
TGTACATAGG GACTACAACA GAATGACGCT CATTATTGAC AGAATCAAGT TCAAACCTCT	180
TGTCCTGGCG TCTGTTGGCC TCTGGCAGCT GGTCATCTG GCATTAGCTG GTTGACAGAG	240
TTGCTGCAAC CCTCCCACCC CGCTCGAG	268

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 463 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GTGAGGTTTT AACTGAGCTC GAAGAATTGG AATCAAAAGA GATAGGTTTG TCTCAGTCCA	60
GACAGTGGAT AGCATAAGGA AAGTACAAC GCAGAAAAGA GGGGGACAGC GAAGAGACTG	120
GATTGATGCG TTATCTAGGC GGTACCTGTC TCCATTCTTT TCTAGCCAGC CTTTGAGCAT	180
TTCATCAAGA ATAGAGGAAT TCAAAGTACT GCAGTCTGCT TGAACCAAGT CTTGTGAGTG	240
GCTCTAAAAA AAATACTTGA ATTTGAACTT GAAAGAACAC TCAAATAAGG TTTGGGGCTT	300
CTCTTTGTTT AATACTTTAA GCGTCTTATT TCTAACATAA ATATACTGAT TGCACAGAAT	360
TTGATTGTTT ATAGCAGCAG TTGCCTGTAC TTTAGAATTC TCAGATATTA GAGCTGAAAG	420
ATCATCTGAG TTACTTTATA AATGGGGAAA TCTCGATCTC GAG	463

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 451 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAACGGCAGC	CATTGAAGCA	TATTGGAAAA	GGAAGTGGGG	AATTTATTAA	AGCACTCATG	60
AAGGAAATTC	CAGCGCTGCT	TCATCTTCCA	GTGCTGATAA	TTATGGCATT	AGCCATCCTG	120
AGTTTCTGCT	ATGGTGCTGG	AAAATCAGTT	CATGTGCTGA	GACATATAGG	CGGTCCTTGA	180
GAGAGAACCT	CCCCAGGCAC	TTCGGCCACG	GGATAGAAGA	CGGCAGGAGG	AAATTGATTA	240
TAGACCTGAT	GGTGGAGCAG	GTGATGCCGA	TTCCATTAT	AGGGGCCAAA	TGGGCCCCAC	300
TGAGCAAGGC	CCTTATGCCA	AAACGTATGA	GGGTAGAAGA	GAGATTTTGA	GAGAGAGAGA	360
TGTTGACTTG	AGATTTTCTA	CTGGCAACAA	GAGCCCTGAA	GTGCTCCGGG	CATTTGATGT	420
ACCAGACGCA	GAGGCACGAG	AGCCCCTCGA	G			451

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 513 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GAATTCGGCT	TCATGGCCTA	CTCAGATCTT	AAAATTCAGG	CTGTCAAAGA	GATTTGCTAT	60
GAGGTTGCTC	TCAATGACTT	CAGGCACAGT	CGGCAGGAGA	TTGAAGCCCT	GGCCATTGTC	120
AANATGAAGG	AGCTTTGTGC	CATGTNTGGC	AAGAAAGACC	CCAATGAGCG	GGACTCCTGG	180
AGGGCAGTGG	CCAGGGACGT	CTGGGATACC	GTCGGTGTG	GGGATGAGAA	GATCGAAGAC	240
GTCATGGCCA	CTGGGAAAGG	CAGCACTGAT	GATAGTGACC	TCAAGGTTCA	TATAGACAAG	300
CTGGAAGATA	TTTTGCAAGA	AGTCAAAAAG	CAAAATAACA	TGAAAGACGA	GGAGATAAAA	360
GTCTTAAGAA	ATAAAATGCT	CAAAATGGAA	AAAGTCTTGC	CACTGATCGG	ATCTCAGGAA	420
CAGAAAAGCC	CAGGAAGCCA	CAAAGCAAAG	GAGCCTGTTG	GTGCTGGTGT	TAGTAGCACC	480
TCTGAGAATA	ATGTAAGTAA	AGGAGACCTC	GAG			513

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CAGAATGGGA	TCGAAGCCTG	CCTCCTTAGG	NTCTTTGCCN	TCATCCTCTC	TGGCAAATGC	60
AGTTACAGCC	CGGAGCCCGA	CCAGCGGAGG	ACGCTGCCCC	CAGGCTGGGT	GTCCCTGGGC	120
CGTGCGGACC	CTGAGGAAGA	GCTGAGTCTC	ACCTTTGCCC	TGAGACAGCA	GAATGTGGAA	180
AGACTCTCGG	AGCTGGTGCA	GGCTGTGTCG	GATCCCAGCT	CTCCTCAATA	CGGAAAATAC	240
CTGACCCTAG	AGAATGTGGC	TGATCTGGTG	AGGCCATCCC	CACTGACCCT	CCACACGCTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GAATTCGGCC	TTCATGGCCT	ACTTCATTGT	AAGGTACTTC	TTTGC GGCGC	TGACAGTGCT	60
CACGCTCCTG	GGCCTCCTCC	ATGGACTCGT	GCTGCTGCCT	GTGCTGCTGT	CCATCCTGGG	120
CCCGCCGCCA	GAGGTGATAC	AGATGTACAA	GGAAAGCCCA	GAGATCCTGA	GTCCACCAGC	180
TCCACAGGGA	GGCGGGCTTA	GGTGGGGGGC	ATCCTCCTCC	CTGCCCCAGA	GCTTTGCCAG	240
AGTGACTACC	TCCATGACCG	TGGCCATCCA	CCCACCCCCC	CTGCCTGGTG	CCTACATCCA	300
TCCAGCCCCT	GATGAGCCCC	CCAGGTCCTT	CGAG			334

## (2) INFORMATION FOR SEQ ID NO:378:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GGATTTTAAG	GATCACATTC	CAAGGGAAAC	TGATATGAAG	GTTGCAATGA	ATGTGTATGA	60
GTTATCATCA	GCTGCCGGAT	TACCTTGTGA	GATTGATCCT	GCATTGGTCG	TAGCTCTTTC	120
TTCACAAAAA	TCGAAAACA	TTAGTCCAGA	AGAAGAGTAT	AAAAATGCCT	GCCTTCTCAT	180
GGTGTTTGTG	GCAGTTTCTT	TGCCAACACT	GGCCAGTAAT	GTGATGTCTC	AGTACAGCCC	240
TGCTATAGAA	GGCATTGCA	ACAACATACA	TTGCTTGGCC	AAAGCCATCA	ACCAGATTGC	300
TCGAG						305

## (2) INFORMATION FOR SEQ ID NO:379:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GAATTCGGCC	TTCATGGCCT	ACCCAAACAT	TATCCCTCTA	CACTGTCCCC	ACTATGCTAT	60
ACCCCTGCAC	TATACCCCTA	TGCTGTCTCC	CITACGCTAT	CCCCCTATGC	TATGTCCCCT	120
ACACTATCCC	CCTTTGTTGT	CCCTCCATGC	TACTCCCTAC	GCTATCCCAC	TACTCTATCC	180
CCCTGACGCT	GTCCCCCTAC	GCTATCCCGC	TACACTGTTC	CCCCTACACT	ATCTCCATAC	240
ACTGTCCCCC	TACACTCTCC	CCCTACTCAA	TTCCCCCTAC	ACTCTCCGCG	TACACTATCC	300
CCGTACACT	ATCCCCCGAC	GCTCTCGAG				329

## (2) INFORMATION FOR SEQ ID NO:380:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GTTGGAATGC TCTTTACTTC CTTTGTGGAG CCTCCCTGCA CAAGCAGCAC TTTCTTTTGC	60
CATAGCAACA TGTGCATCAA TAATTCTTTA GTCTGTAATG GTGTCCAAAA TTGTGCATAC	120
CCTTGGGATG AAAATCATTG TAAAGAAAAG AAAAAAGCAG GAGTATTTGA ACAAATCACT	180
AAGACTCATG GAACAATTAT TGGCATTACT TCAGGGATTG TCTTGGTCCT TCTCATTATT	240
TCTATTTTAG TACAAGTGAA ACAGCATCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 338 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GAATTCGGCC TTCATGGCCT ACATAACTCT CCACAGGCTC CCCTGGGAGG GGTGCCCCCA	60
CCTCACCCGC CACCTCACTT CTCAGCCCCT CTTCCCATCC AAGGGCTCCC TGGGCTGCCC	120
CCACCCTAGT CATGATCTCG CTCCTCTACT CTCTCGTAGT ACTTTATTTT TACCTTGCTC	180
CTGGCTCACA TTACATGCTT ATCTTGTAAT TATAGATGGT TCTACATATG TCTCCTTTTG	240
CATCCTTTTC TCAAAGCTCC TGTGAGGCCA GGGATGGTTT TATGCCTTTT CTCATCCCCT	300
TATGTTCTAG TATAATGCTT TACACATGTT TACTCGAG	338

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GAATTCGGCC TTCATGGCCT ACTTCTCTC CTTTTTCCT GTAACGTGC TGGTTTTGTT	60
TTGGTCTTCC TCTCATACCC GTTCTGTCAT TTCATCTTTT CTTTCTATTG GGACTTCATT	120
TCATTTTTTT TTAACCTTAT CTTTGTTTC TCTTGTTTAT CCCATCCTTT TTGATAAAAT	180
CCATCGCATG TGTCTTCTTT TTTTCTTTAT TTTCTTTCCT TTCCTTTTTT CTTTTTCTTT	240
CTCCCAAAC TTTTCTTTT CACAGCATTG GAACACGGA GGTAGTCACC CAGAAGAAT	300
TGAGCGGCT GGTGCCCATC CGAGACCACT CGAG	334

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GCAGAAAATA TGGTATCGGT TTCATTTAAT AAAAATGAAA AAATAATTTT CAGTTATCAG	60
TAATTTCTCA GTTACACAAC CTCTGCCTTC ATTTCCGCTT AGCCATGAAC TTTTACTGC	120
ACAAAGGAAT TTAATAATAGC CAAATTCTAC AATTCTGGCT GGGTGTGGGG GCTCATGCCT	180
GGGATCTCAG TAGTATGGGA CCCCAGAGCA GGTCTAGAAT TCAATCCTCG AG	232

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GCCTCTGCTT TTAATTCATT GGCAACTGTT ACGATGGAAG ACCTGATTCG ACCTTGCTTC	60
CCTGAGTTCT CTGAAGCCCG GGCCATCATG CTTTCCAGAG GCCTTGCCTT TGGCTATGGG	120
CTGCTTTGTC TAGGAATGGC CTATATTTCC TCCCAGATGG GACCTGTGCT GCAGGCAGCA	180
ATCAGCATCT TTGGCATGGT TGGGGGACCG CTGCTGGGAC TCTTCTGCCT TGGAAATGTC	240
TTTCCATGTG CTAACCCTCC TGGTGCTGTT GTGGGCCTGT TGGCTGGGCT CGTCATGGCC	300
TTCTGGATTG GCATCGGGAG CATCGTGACC AGCATGGGCT TCAGCATGCC ACCCTCTCCC	360
TCTAATGGGT CCAGCTTCTC CTGCCCACC AATCTAACCG TTGCCACTGT GACCACTT	420
CTCGAG	426

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GAATTCGGCC TTCATGGCCT AGGCCCTTAA ACTGGATTCA AAAAATGCTC TAAACATAGG	60
AATGTTTGAA GAGGTCTTGC AGTCTTCAGA TGAAACTAAA TCTCTAGAAG AGGCACAAGA	120
ATGGCTAAAG CAATTCATCC AAGGGCCACC GGAAGTAATT AGAGCTTTGA AAAAATCTGT	180
TTGTTCAAGC AGAGAGCTAT ATTTGGAGGA AGCATTACAG AACGAAAGAG ATCTTTTAGG	240
AACAGTTTGG GGTGGGCCTG CAAATTTAGA GGCTACCTCG AG	282

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GATTGAATTC TAGACCTGCC TCGAAGGCCG AGAGGGAAAG TTGAAAGGTC CCAAATTC	60
GATGCCTGAG ATGAACATCA AAGCCCCCAA GATCTCCATG CCTGACATTG ATCTTAACCT	120
GAAAGGACCC AAAGTGAAGG GTGATATGGA TGTGTCTCTG CCAAAGTGG AAGGTGACAT	180
GCAAGTTCCT GACTTGGATA TTAAAGGCC CAAAGTGGAT ATTAATGCCC CAGATGTGGA	240
TGGACTCGAG	250

## (2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

GAATTCTAGA CCCACCTCCA CCTTTAACTC GAAGTAACAC TGCAAATCGT TTAATGAAAA	60
CACTCTCAAA ACTGAATTTA TGTGTTGATA AAACAGAGAA AGGAGAAAGT AGTAGTCCTT	120
CTCCATCAGC TGAAAAAGGA AAGATTCTAA ATGTTTCAGT GATTGAAGAA AGTGGCAATA	180
AAAACGATCA AAAGTCTCAA AAAATTATGA AGAAGAAAGA GTCATCTTCT ATGTTGGCTA	240
CAGTTAAAGA AGAAGTCTCT GGTAGTTCAG CAGCTGTTAC GGAGAATGCT GATAGTGATA	300
GAATTCTGA TGAAGCAAAT AGTAATTTTA ACCAAGGGCT CGAG	344

## (2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

GGAGTAATCA GAGGTGTTCT TGTGTTGTGA TAAGGGTGGC AGGAGTGGAC ATTCTTCACA	60
TACACCCATT ATTGTTTGA AGTGTTTAAT TACCTTTTGA GCTACATTTT TGCAGCTGAG	120
TTAGAAATGA AAACCACAAG AGTTTATTG TTGGCTGTAC TCGAG	165

## (2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GAATTCGGCC TTCATGGCCT AGAACAGAGC TTAATTATTC TTCTGAAAC CAAGGCTTCT	60
CTAGTGAGCA CCATGAGCCT TTGGAAACAA CAGATGTATA CAATAGCAAA GTTTCATTTT	120
TTTACCTTGA AACGTGAAAG TAAATCAGTG AGATCAGTGT TGCTTCTGCT TTTAATTTTT	180
TTACAGTTC AGATTTTTAT GTTTTGGTT CATCACTCTT TAAAAATGC TGTGGTTCCC	240
ATCAAACCTCG AG	252

## (2) INFORMATION FOR SEQ ID NO:390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

GAATTCGGCC TTCATGGCCT AGGATGTTCA CTGTCATGCC TCTGGATTTT AAAATTATTG      60
TTCACATGAC TCCTTTTCTG TGCCTTGGGA AGCAGCTACA GAGCAGTAGA ATCCACTGAA      120
TTGGTACACT GAAGCAGGCA TGCCATTAA ATGAAGGCAG TTAACCTTGA CTGTTGTATC      180
ACCAGAGTTA AAGAATTCTG GTGCCCCTCT TTAAGTCTTC AGGAAGTGTT TAGAGGCTTA      240
TTCACATTAG TTAAACAGG CCCCCCCCAC CTTCCCCAAG GCAACAGAAA ACATAACCAT      300
TAGCTCTCTT CCTGTTTTCC TTCCTCATT CATGCTTGCT TCGGCTGCTA AACTGAATTT      360
TTGTACTTA GAATATTATA AAGTGTGGAT GCTTCTATA ATGCTATTGG TCTAAGTGTG      420
ATTAAATTTC ATTAAGGTGT ATAAGCTCT AATTATTACA TAACTGGCAC TGGCTCGAG      479

```

## (2) INFORMATION FOR SEQ ID NO:391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

GAATTCGGCC TTCATGGCCT AGCCTATTAC ACAGTAAGTT AATAATTGTG TCCTTGCAA      60
TAAGCATTGT GTTCTGAAAT GGAATCAGCA TATTCCCTA TAAAGACACT TCCACTCATT      120
CATTAAATTGA GCAGCCCCAG TTGATAAAGA ATCAGTATAT CATGTTCTGA TATTTAATCA      180
GCAAACTCAT TTATTCAGTA GAAATTTGAA TTCCTGTGAT GTGCCAGGCT TGTGAGGAGG      240
GAGACTCGAG                                     250

```

## (2) INFORMATION FOR SEQ ID NO:392:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

GAATTCGGCC TTCATGGCCT AGTCGACTCC TGTGAGGTAT GGTGCTGGGT GCAGATGCAG      60
TGTGGCTCTG GATAGCACCT TATGGACAGT TGTGTCCCCA AGGAAGGATG AGAATAGCTA      120
CTGAAGTCCT AAAGAGCAAG CCTAACTCAA GCCATTGGCA CACAGGCATT AGACAGAAAG      180
CTGGAAGTTG AAATGGTGGA GTCCAACTTG CCTGGACCAG CTTAATGGTT CTGCTCCTGG      240
TAACGTTTTT ATCCATGGAT GACTTGCTTG GGTATGGAGA GTCGGCTTGA CTACACTGTG      300
TGGAGCAAGT TTAAAGAAG CAAAGGAACT CCTCGAG                                     337

```

## (2) INFORMATION FOR SEQ ID NO:393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

```

GCGATTGAAC TCCTGACCTC AAGTGATCTG CCCACTTGTG CCTCCCAGAA CTGGGATAAA      60
AAAAAAAAAA ATAGATCCTT GGTATTATTC CATTACATAC GGATTGTAAA ATTCAGTTAA      120
ACATTTCATCT CTTGGTGGGC ATTATGTAT TTCTTTTGTG TGTGTTGTTG CAGCATGCT      180
CTGTAAACC TTTTATAAG TACATCTCGA CTCGAG      216

```

## (2) INFORMATION FOR SEQ ID NO:394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

```

GAATTCGGCC TTCATGGCCT ACCACATTG TAACGGAGCC ATTGAAGCAT ATTGGAAG      60
GAATCTGGGA ATTTATTAAA GCACTCATGA AGGAAATCC AGCGCTGCTT CATCTTCCAG      120
TGCTGATAAT TATGGCATTG GCCATCCTGA GTTCTGCTA TGGTGCTGGA AAATCAGTTC      180
ATGTGCTGAG ACATATAGGC GGTCTGAGA GCGAACCTCC CCAGGCACTT CGGCCTGGGA      240
TACTCGAG      248

```

## (2) INFORMATION FOR SEQ ID NO:395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

```

GAATTCGGCC TTCATGGCCT AGCCTTCCTC TACCATTTT AATTTTTTTA GACTTCATT      60
TGTGATTTAT TGCTGCTCTG GGGGCTTCAC ATCCAATCCT TTTATGGTTT CATCTTTCCT      120
TTCCTTACAT TTGTTGCATA TAACAATGGC GTGTTTAGCT ACTGCAGTGA AAAATCAATC      180
AAGCCTATTC CATATTCACA GGCTTGCAAT GGCACCAACG GCTCCTGGAT CTCCTCGAG      238

```

## (2) INFORMATION FOR SEQ ID NO:396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC TTCATGGCCT AAGTTGATCC GGATACACAC CTGCTAAAAC TGCTTAAAAC	60
ATTAGAAGGA CATGCTTATG GCGTTTCTTA TATTGCATGG AGTCCAGATG ACAACTATCT	120
TGTTGCTTGT GGCCAGATG ACTGCTCTGA GCTTTGGCTT TGGAAATGTAC AAACAGGAGT	180
CTCTCGAG	188

## (2) INFORMATION FOR SEQ ID NO:397:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC TTCATGGCCT ACAGGCATGT TGAGATTGG AAAAGTGGAT GTAAGTGA	60
TTCAGATAGC TTTAGTGATT GTCTTTGTGT TGTCTGCATT TGGAGGAGCA ACAATGTGGG	120
ACTATACGAT TCCTATTCTA GAAATAAAAT TGAAGATCCT TCCAGTTCTT GGATTTCTAG	180
GTGGAGTAAT ATTTTCCTGT TCAAATTATT TCCATGTTAT CCTCCATGGT GGTGTTGGCA	240
AGAATGGATC CACTATAGCA GGCACCAGTG TCTTGTCACC TGGACTCCAC ATAGGACTAA	300
TTATTATACT GGCAATAATG ATCTATAAAA AGTCAGCAAC TGATGTGTTT GAAAAGCATC	360
CTTGTCCTTA TATCCTAATG TTTGGATGTG TCTTGCTAA AGTCTCACA AAATTAGTGG	420
TAGCTCACAT GACCAAAAGT GAACTATATC TTCAAGACAC TGTCTTTTGG GGGCCAGGGC	480
TCGAG	485

## (2) INFORMATION FOR SEQ ID NO:398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCGGCC TTCATGCCTA GTGGATCCGG AACTCTGTG GCTCTAGACT TTCAACTATT	60
TTATTTTTC TTTTGATTT TTTGTTGTT GCTTGCTTTT TTACAATGGG AACTAGAATG	120
TAAGATGCCA AACTCAGCCT GTGGGAACA TGGATTTTCA CAACAGCAAC CACAGAGCGT	180
GGTTTCCATT TCTATTCCCT GTTCATGTGG GAGGCAGAGA AGGAAATCAG GTGCTCAGTT	240
CCAGGGACAT CACAGGACAG GACTCGAG	268

## (2) INFORMATION FOR SEQ ID NO:399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:



```

GAATTCGGCC TTCATGGCCT ACACCTCTTC TGCCAACCAG CTGCTTGGGA TGA CTGCGAT    60
CCCGTGTGCT TGTCTGGGTA TCTTCCTGGG AGGTCTTTTG GTGAAGAAGC TCAGCCTGTC    120
TGCCCTGGGG GCCATTCCGA TGGCCATGCT CGTCAACCTG GTGTCCACTG CTTGCTACGT    180
CTCCTTCCTC TTCCTGGGCT GCGACACTGG CCCTGTGGCT GGGGTTACTG TTCCTATGG    240
AAACAGCACA GCACCTGGCT CAGCCCTGGA CCCCTACTCG CCCAAG                    286

```

## (2) INFORMATION FOR SEQ ID NO:400:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

GAATTCGGCC TTCATGGCCT ACCTGCCTCG AGATGATCAT TCTTTTCTTG CTTCTAGGCT    60
CTGTGTCCTC CTGTTTTCCT CCAACCTCTC TGTCCTGTG TCATTGCTG TGGGTTCTTT    120
TTGCCCTTGC CACCCCTCAA ATGGGGCTTC TCACTCACAC TAGTGAGTTT TCAGTGCTTG    180
CAGACCCAAC ACCCTCTTTT TATAACAAAT ATTTTTTAAT ACGTCCTTTT CCACAACCTG    240
AG                                242

```

## (2) INFORMATION FOR SEQ ID NO:401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

GAATTCGGCC TTCATGGCCT AGTCCCATCA GAGGGAGCTG ATGAAGAATG GTCCCTGTAA    60
GTAAGTCACT AGGTCAACA ACTGCCTGGC CGAGCACTCA GCCCGTGGAG CTCAGGCCAA    120
CACCAGAGCC CCGGTTT TAG GGGCCAGGAG AGCAGGTGAC CAATTATTG GGGAGTCTTG    180
GGTAGAATTT CCGCCACACA TTCTCCCAG GGCTGCAGGG GTCTTCCGAG GCAGGGCGGT    240
GGAGCAGGAT TCAGGATGTG GTGGAATAG AGTGAGGGGC AGTGGGTGGT GCTCGAG    297

```

## (2) INFORMATION FOR SEQ ID NO:402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

```

GAATTCGGCC TTCATGGCCT AAAAACTAG AATAATGGAA GAGTAAATAA ACACAATTCT    60
TAATGTATTA CAAGAAATAA AAGGTTTAAA AGTAGATTTT TTAATTGAAA AGAATTAAAT    120
CAGATAAAAA TATTTGAGAG GTAATGCAAA CATTTAAGTT TGTCAAAGAA GCTTCAACAT    180
CTGGATAATA GGAAAGAAAA AAACCAAGC AAAAGAAAAA TAAGCCACAA ACTAAAAAAT    240
GTTTAGTTCT TGAAATTAA AAAAGTAAAT ATTGAAAGAG CATGCTGTGT ACCTGAGATT    300

```

ATTTACCCAA AACTCGAG

318

## (2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```

GAATTCGGCC TTCATGGCCT AGATTGAATT CTAGACCTGC CTCGAGTCTG GGCACCCTGA      60
GCAGCAGCCT GAGCCGGGCC AAGTCTGAGC CCTTCCGCAT TTCTCCGGTC AACCCGATGT      120
ATGCCATCTG CCGCAGCTAC CCAGGGCTGC TGATCGTGCC CCAGAGTGTC CAGGACAACG      180
CCCTGCAGCG CGTGTCCCGC TGCTATCGCC AGAACCCTTT CCCCCTGGTC TGCTGGCGCA      240
GCGGGCGGTC CAAGGCGGTG CTGCTGCGCT CTGGAGGCTT GCATGGCAAA GGTGTCGTCTG      300
GCCTCTTCAA GGCCAGAAC GCACCTTCTC CAGGCCAGTC CCAGGCGGAC TCGAG          355

```

## (2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 346 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```

GAATTCGGCC TTCATGGCCT AGTCATGGAA CAAGTCCTTG CTAAACTAGA AAACAGGACT      60
AGTATTACTG AACAGATGA ACAAAATGCAA GCATATGATC ACCTTTCATA TGAACACCT      120
TATGAAACCC CACAAGATGA GGGTTATGAT GGTCCAGCCT GGGTGACAGA GCGAGACTCT      180
GTCTTATAAA GAAAAAAAAA AAAAGAAGTG GCAGCTCTGT CTGCTTCTCA CAGAGTTGCT      240
AGGGACAAC TCTGAGGCAG GCACCTGCC TTTGGGCTCCC CGGGTGGGCT GCTATTTGCC      300
TGTGGGCTCT GCCTGCCCGC CTGTCCAGTC CCCGGGGTGG CTCGAG          346

```

## (2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

GCGATTGAAT TCTAGACCTG CCTCGAGAAC AGGGAACCTT CAAACAAAAG ATATATCATA      60
GGAAGTCAGG TGAGAAGCTG TCAACTGGGC AGGCAGTGAT GAGAATCGTA GTTGTCTTAC      120
TGTACTTTTT TGTTTTGTTT AAAAAACCTA AAGCATCACG CATTTTGAAA GCAGAGTTTG      180
CAGAGAGCCC CCAACAGAGC CAGAACTTGC CAAGAGCGAC TGATATTTCT AGAATCCCA      240
GAGGCAG          247

```

## (2) INFORMATION FOR SEQ ID NO:406:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

GAATTCGGCC TTCATGGCCT ACAACATCAA AACTCCCAAG CAAATGGATG AATTCATTGA      60
GATCCAAAGT TCAACAGGAA CCTGGTACCA GCGCTGGCTG GTCAGATTCA AGACCATTTT      120
CAAGCAGGTC TGGGATAATG CCTGTACTG TGTGATGGG CCCTACAGAA TGAATACACT      180
GATTCTGGCC GTGGTTTGGT TTGCCATGGC ATTCAGTTAC TATGGACTGA CAGTTTGGTT      240
TCCTGATATG ATCCGCTATT TTCAAGATGA AGAATACAAG TCTAAAATGA AGGTGTTTTT      300
TGGTGAGCAT GTGTACGGCG CCACAATCAA CTTACGATG GAAAATCAGA TCCACCAACA      360
TGGGCCTCGA CCTGACTTIG CCCCTTGCC CATCAGCCAT TGGCCATCAC CCCAAACAAC      420
TCAGCTTCGG GGAAGTCTCG AG                                         442

```

## (2) INFORMATION FOR SEQ ID NO:407:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

CCGAGTGACC TTCTTGATGC TGGCTGTTTC TCTCACCGTT CCCCTGCTTG GAGCCATGAT      60
GCTGCTGGAA TCTCCTATAG ATCCACAGCC TCTCAGCTTC AAAGAACCCC CGCTCTTGCT      120
TGGTGTTCCT CATCCAAATG CGAAGCTCCT CGAG                                         154

```

## (2) INFORMATION FOR SEQ ID NO:408:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

```

GAATTCGGCC TTCATGGCCT AGTTTACTTC TGCTTGATCT TTATCTTCC TTGCTACTAA      60
TTTTGGATT AGTTTGTCT TTTCTAGACA TTCATTGTTA GATTGTTTAT TTACAAATTT      120
TCTAGTTTTT TTGATGTAGA CATTTA                                         146

```

## (2) INFORMATION FOR SEQ ID NO:409:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCGGCC	TTCATGGCCT	AGATGTTGCC	AGTTTTCATG	GAGGAAGTAG	ACATGAAAGC	60
TTGTTTGTA	TGTGTTTGAC	AGAGTAGAAA	GACATTGAAG	AAGGTGATGG	TATACATCAC	120
TTGAATATT	TTATTGAAAA	GGGAGGGAGG	AAATGGAGCG	TTAGTTGTAG	GACCAGATGA	180
TGTAAAGAGA	GTTTTTTAAA	GTGTACAAAA	CAATGGCATG	TTGTGATACT	AATGAGAAGG	240
AGCCAATAGA	GAACAAAAAA	TTGATGATGC	AGGAGACGAC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CTCGAGGGAT	CTGGCTTTCT	CTGTCTTCTC	ATTACTACA	TNACGCTGGT	GAATTAATAG	60
ATNTCTCAAC	AAAAGGACAT	TTAAATCAAC	ATATGACACC	TGTTTAAATT	CTAAGAAGC	120
CATTAATTAC	ACATTCTTAA	GAAAATGAGC	TATGACACAA	CTCTTCTCAC	TGTATAACTC	180
CTATCTGTGA	TTCTCAATCA	GGTGACTTTT	CAGCTNCAAG	ACGGATCTTT	TCTATTATC	240
TCCTCTGGTT	CGGACCAATT	AAATGNTTTC	TTTTGCAATC	ANAACTCTC	ANNTGCCAAA	300
TCTTCAAAAG	CAAAGGAGTT	NGTTAGCAAC	ATATTAGGCC	ATGAAGGCCG	AATTC	355

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCTAGA	CCTGCCTCTG	TATGTTGCTT	TAGCCAGGAT	TCAGAGCTAA	AGTGTAAAGT	60
TGTGCTTCTG	CTTTCTGGAT	GTATCTCTCA	AAATTGCTCT	GTCTGTTTAT	TCAGCTCCTG	120
GATCTACCTT	CTCTTTTCTT	TGAATTGGAC	ACCATTCATG	TCATTGCTCA	CTCAGAAGTT	180
CAGCTGTTCT	CATGATCACA	TGCTTTCTTC	CCTGTTTATG	TCCAAT		226

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

GAATTCGGCC TTCATGGCCT AGTCTGCTGC TTAGCTTGTA TTTTCAGTTT AATATATTCG      60
TGATCATTAA CAAAACAGCG AAGTGAATAA TGGGCATAAA TTTTCCTAAG AAGAATCATT      120
TTCCATACTT ATTTTCAAT ATTATCAAAA AGTATGTAAT TTTGGGGGGT TTTTGGTTT      180
TTTTTTTTTT TGAAACAGAA TCCTGCTCTG TTCTCGAG      218

```

## (2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 260 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

GAATTCGGCC TTCATGGCCT ACTTTGAACA ATTCGGCATG AATTGAAACC AGGTTTTCTT      60
GTGGAAAGTT ATAGCTTGAT TGGGAGATAG AAGTTGAATT GAGTTCCTTC TTGCAACTCT      120
TAGTGTTTAT TTTTATATCT CAGTAAGACG AGGATACCTT CAGTTTGAAT CTGCATAATG      180
TTCCTGCCA AACTCCTTCT CATTAAATGC TTATGGCCTT CACATTTCTG TATAATAAAG      240
ATCAATTATC AGCACTCGAG      260

```

## (2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

GAATTCGGCC TTCATGGCCT AAGCATATGA ATTTTGGA GAACAGACATA CAGACCATAA      60
CAGTTCCTATT TTCTATAACT ATAGTAGAAT ATCGAAATGA GAACATTGAC ATTGGTAAAA      120
GGTGTATGTA TAGTTTATAT GTTATCTTAT CAAAAGGGTA GATTACAGA ACCAACACAA      180
GTAAGCTATA GAACTAGCCC ATTACCACAA AGATCTCCCA CAAGCTACAG CTTTACAGTC      240
ATACCCACCC GGCTCGAG      258

```

## (2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

GAGGACCTTT ATAATCTACT ACTAATTACT GTGAAAGTAA ACATTGTTTA ATATACCAGT      60
TCITAAAGAA ATATTTTGTC TAGTCATTAA TATTCTAGTT CATCTCAAAG CTTCCATTTC      120
ACAATTTAAA ATTACTTAAA TTTTAATATT AAAGGAAACA GTTTTCCTGA TTCTCATGAA      180
AGTTCCTATT TGCCTGAAG ATGACTAAAC CTTTGTAGTCA TAGTTTTAGA AGAATTGGCT      240
TTTTTATAGC CATTTTATTT ACATATGGGT ACGGACTCGA G      281

```

## (2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```
GAATTCGGCC TTCATGGCCT ACTCAGAAAA GAAATGAAA ATACCTCTAC ATGTGGTCTT    60
CCTGCTAATC TCTCTGACCT TCCTATTCAC CACCCTCCCC ACTGCCCACT TACTCGAG    118
```

## (2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```
GCGAGGATGG CATGGACGCT TATCGAGCAG CTTCAGGGTG GCAGCTACAA GAAGATTGGC    60
TACTATGACA GCACCAAGGA TGATCTTTCC TGGTCCAAAA CAGATAAATG GATTGGAGGG    120
TCCCCCCCAG CTGACCAGAC CCTGGTCATC AAGACATTCC GCTTCCTGTC ACAGAAACTC    180
TTTATCTCOG TCTCAGTTCT CTCCAGCCTG GGCATTGTCC TAGCTGTTGT CTGTCTGTCC    240
TTTAACATCT ACAACTCACA TGTCGTCTC GAG                                273
```

## (2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

```
GAATTCGGCC TTCATGGCCT AAGCAGTTGC TAATGCCAGC AGTACATAAA TTGAGGATGG    60
AGCAAAAGGA TCGACACCAC CAATGGCTGC ATTGTGATAG GTGTGGACAG AGCCTGCCAG    120
AATTAAACAC ACGCCAGGAC TCGAG                                145
```

## (2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

GGATTGGGCC TTCATGGCCT AGTGTTTTATA ATTAATCCIT TAATATTATG GTTATTAAAC      60
TCTTAAACAT GAATGAATTC TTGATTGTTT TAACACAGTA CCTAAGACTA ATGCTTTCTG      120
TGGACACCAC TGAGCTCTGC CTCAACTCCA CCTCTGCGA CCGGAGGACT ATGCCCTTAG      180
TAACTGCTGT CGGTGTGGAC GCTGTGCTGG TTCTGTTTTC TAAAGGAGCA GAAGGACAGG      240
TCTCTGAGAC AGGATCGTTG TCCCTACAGG AGGAACAGTG GCCACTCGAG      290

```

## (2) INFORMATION FOR SEQ ID NO:420:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

```

GCGATTGAAT TCTAGACCTG CCTCGAGCCT CCCAAAGTGC TGTGATTACA GGAGTGAGCT      60
GCCAGGCCCA GCCTACAAGT TTTTCTTTAA CTACTGCTTT AGTCAACCAT ATCCTCTAGC      120
TTCTGATATT TTCATTGTTT GTTGTCATT TCTAGATATT CAACAATTTC AAATTAGATT      180
TTCTCTTCGA CTAAAGTGGA AGAATTTTTT CCCGTTTATT TTCTACATGC TAAAGATTTT      240
TATTTTCATT TTGTTATTAA TTTCTAGTGT TACCGTATTG TCATTAGAAA ATATGGGCTG      300
GCTCGAG      307

```

## (2) INFORMATION FOR SEQ ID NO:421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```

GAATTCTGAA AATATTAAGA TTTATCCTAG CACTTACGTT CAACATACCA TAATTTTTTAT      60
ACTTCTCCAT CTAAATAAAA CCAAGTTTGT TCCTACACTA GTCCAGCCTG CATCTCTAAG      120
AACTCCAGTG ATTATACATC AACATCTAGA GATCAGGTAT CCCAATCCTT TCTTCCTATA      180
TCTAAGCTAA CTCCTTCTTA GCCAAATGGT ACCCTTTGAT TTTGTGTTAA TCCTTTCCCTT      240
CCCTCCACTC TTAACCCCTC TCATTCCATC TTCTCCCTCC CTTTCCACC CCACTCTCGA      300
G      301

```

## (2) INFORMATION FOR SEQ ID NO:422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

GAATTCGGCC TTCATGGCCT AGGTAAAGT TGTCTGGTAA TAAGGTGGAG TGGATTGGG      60
GCAGGTTTTA TGTTTGTGTG CTTCTCTTAG AAGTCAAAGA GTTGGTGAGG TAACTGCAAT    120
CCTGTCTATA TCAGTGTAGT GATAATGCAC TAGTGTAATG AAGAATGGAG CTGCACGTGT    180
GAGGTTTTTC AAGTCCACAA AGATCAGGTA TTGTCTACGG TCAATAAAGA TTTTTTTAAA    240
AAACCCTCTT AACTAAAGAG AGGTAAC TTCCTTCAAAA CTCTGAAAT TACATGTGCT      300
GACTTATAAT ATGTGTGATC CTCGCTGCTT TTCGATCCC TGGTGGTTGG GGTGTGTGTG    360
TGTGTGTGTC TGTGTGATGG GCTCTCGAG      389

```

## (2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```

GAATTCGGCC TTCATGGCCT AATCTTAAGT GTTTTACATG CTCTACCTGC CGGAATCGCC      60
TGGTCCCGGG AGATCGGTTT CACTACATCA ATGGCAGTTT ATTTTGTGAA CATGATAGAC    120
CTACAGCTCT CATCAATGGC CATTGAATT CATTTCAGAG CAATCCACTA CTGCCAGACC    180
AGAAGGTCTG CTAAAAGGTC AGAGTAATGC AGAATGCGTG CCTTCATCTC AGATTGTGTC    240
ATCACAGGTG GATCCCATGT GTCTTCAGTA GACAAGTCAC CTTGTAGCT AGCACCAGTG      300
CCAGCTCCAT GCCATTGCAC CTCGAG      326

```

## (2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

GCGATTGAAT TCTAGACCTG CCTCGAGCCA ATCATTTTTA AATCTAATCT GAACTTTAAC      60
TGGTTAGTTG AGTGCATTTT TATGTGTACT GATGTATTG CATTATTCC TTACCACCTT    120
ATTTTGTGCT TTTTATGTTT TTTTCTTCCA CTCITTTTTT TTCTTTTGA ATCTCGAG    178

```

## (2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

```

GAATTCGGCC TTCATGTACA TAGATCTTCC TAGTGTCAAT GACAAAGGTG ACATTTGCAA      60
GGCTTTTCT TCATCAGATG CAGGGATCTG GACTTCATGT GTATCCTTTT ATCCACTCCT    120
CTCGAG      127

```



## (2) INFORMATION FOR SEQ ID NO:426:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

GAATTCGGCC TTCATGGCCT AGAATTTAAT TGCAGAAAAT TATTCATATT CTTATAATCC      60
TTTTAATGTC TATAGGATTT ATGATGATAT CTCCTTCC ATCCTGATTT TTTCAAGTTT      120
TTGTTTTTTC TTTTCTTA TAAATCTGG TAAATGTTA TTAATTTTAT TCATTTTAA      180
AAAGAACCAG CTTTGGTT CATAAGTTT TATAATTTT TTGTTTCAC TTTCAATTAAT      240
TCTACTCTTT ATTATTCCT TCATTTGTT TACTTGGGT TTGTTTGCC ATTTTTC      300
TAGTTTCTTA AGGTGCCAGC TCGAG                                         325

```

## (2) INFORMATION FOR SEQ ID NO:427:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

GAATTCGGCC TTCATGGCCT AGGCACACAG GCGGGCAGC AACATAAACG GCACCCATTA      60
AAAAGCAAGA CTCGCTCTTG AGACTAAAGG AGAAGTTACC TAAATTTCTG TATAAACTCA      120
GTAATTCATT CACTTACTA GTATTACATT TATGAAATC ACCTTGTGG AAAAAGGAGC      180
GGGAGAGGGA TAAGAAAATG CCTGTTCTA GAAAACGCTC GAG                                         223

```

## (2) INFORMATION FOR SEQ ID NO:428:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```

GAATTCGGCC TTCATGGCCT AAATTCATAC AGAAGACCTT ATTGTGATAA AGTTCAACGG      60
TATAGGTAAA CAACAACAAA AAAACTATCA ACCATAATTT TTTCACCCTA CCAACATTCT      120
CTGAACCTTT CAGTAATATT TTATACACAT GTGCATATTC TGCCTTTTTC ATTTACTATA      180
TCATAAACTT CTTCTAGAT CATTATTTT CTGCTGCATT TTTCAGGAT TTATCACCTT      240
TATTTTGTAGT TTTAGTTTTT GTGAGTGTAC TCTCGAG                                         277

```

## (2) INFORMATION FOR SEQ ID NO:429:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

AAATGAGCCC	TATCACTGAG	AAATACGTGT	TTCATGATTT	AACTCTGTGT	GTGTGTGTGT	60
GTGTATTTT	TTTTTGGTGT	TCTTCAGCTG	ACAGTATGAA	AAATGAAACT	GCTGAAAAAG	120
CTGAGCACCT	GGTCACCCCT	GGCCTTCCAT	TGCTTTGGCC	TTCAGTAAAA	AGCAGCCTCC	180
CTTCTAGGTC	AGGGAACCAT	GCCATTGAGA	CTAGTAACGG	GCGTTCTGGG	CACAGTCCCA	240
CTGTGCACAG	GTTTGAGAGG	ACAAGTTCAT	CAGAAGGAAG	GCAGTCCTTA	GAAGTCACAT	300
ACGTTGAGCC	CCTCGAG					317

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCGGCC	TTCATGGCCT	ACATTCAGAA	AACAGAAAAG	TTTCAAGAAG	CAGGAAGAAA	60
AGACTCACCT	ATGATCCCAA	CACCCAGAGG	TAATAATTTA	CCATTTTGG	TGTATCTTCT	120
TTGTCTTTTC	CTATGTGTGT	CCTTATGTAG	ATATGTAACA	GGTTGTGGTT	TAAACCGAAG	180
CTATACCCAT	TGTTTGGAGT	CAGGCAGGTG	CGATAAATTT	GTAGGTGGCT	CACCAGAAAT	240
CTATTTGCAT	GATGAACCTA	CAGGACTCGA	G			271

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 349 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GAATCATTTT	TGGTCACCAA	TCTCTCATAT	ACCACTACTG	GATATTTACA	ACATGCTTCA	60
GTGGAGGAGA	AGACACTGCT	GCTTTGCAAA	GATGACCTGG	AATGCCAAAA	GGTCTCTGTT	120
CCGCACTCAT	CTTATTGGAG	TACTTTCTCT	AGTGTCTTCT	TTTGCTATGT	TTTTGTTTTT	180
CAATCATCAT	GACTGGCTGC	CAGGCAGAGC	TGGATTCAAA	GAAAACCCCTG	TGACATACAC	240
TTTCCGAGGA	TTTCGGTCAA	CAAAAAGTGA	GACAAACCAC	AGCTCCCTTC	GGAACATTTG	300
GAAAGAAACA	GTCCCTCAAA	CCCTGAGGCC	TCAAACAGCA	ACTCTCGAG		349

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```
GAATTCGGCC TTCATGGCCT ACCTGGATTT CTCAATTTAT TAAGTTGTAC TTACCTGATG      60
CTGATGATGA TTAGTGATAT TACACATTGT CTCAGAGCTC ACTCTTGCGG AGGTTGTGGC      120
CTCGAAAATG CCTTGTGTGC CCTCTGGAAT CTGTCTTTTC AGCTTCATCT CCTCCTCCTC      180
ACCTCCTGCT GTGGTGACA GATACCTATA GGCAGGCTCC ATCTCCTCCT CCCCAGCTCC      240
TCCCCTAGTG CACACCTCGA G                                     261
```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```
GAATCTAGA CCTGCCTCGA GTCCTACGGG AAACCTCCAG GGTTTTAGGA AGCTGACGAT      60
GCAAGTTTAT CCAAATGGGA ATGATAATAA TCATGTTTAT TATCCTGGGG TGCTTCTCCT      120
ATAGCAAGTA CTCACTTAGG TCCTGTTTAT TAGTCAGTCT TTTAATCTGT ACTGAAATAG      180
GTGCTGTCGC ATCCATGGGG AATGAACTCG AG                                     212
```

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```
GGTTGCAGTG AGCTGAGATC GCACCACTGC ACTCCAGCCT GGGCAACAGA GTGAGACTTC      60
ATCTCCAAAA AAAAAAAAAA AAAAAAAGA CAACCACAAC AAAAACGAAA CACCACCACC      120
AAAAAAGTTT ACTGGTAGAG TCTCCTCTAG ATTGTTTTCT TTTCAATACT TGTTTCATAT      180
TCTCCAAC TG CCCTCGTCCC ATAATGTTGG CTGTGCTTTT CTTGTGCTT ACAGCTCATT      240
GCTGGGATGG ATATGGTGAG TTTTCATGTA CATTGACCAA ATACAATCTC GAG          293
```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```
GAATTCGGCC TTCATGGCCT AGGCTTGAAA GGAAATGAGG GAAATTTTCTG TGAGTTTGAG      60
```

GAATGGCAGA	CTGGGTATGT	GACAAATGAG	TGGGTAAATA	AGGAAATCTC	AGATTGAGAA	120
TCCTGGCAGA	TCTTTCAATG	GGTTAGACTG	CAGGAATATT	GATTTTAAAG	CCAGACTGAA	180
GCAAATTTCTA	GTGATAAAGG	AAGGGGAAAG	GGTGGCTGAA	TCAAATGTTC	TACCAATACT	240
CCTTTTTTTTA	GTATTTGAGT	TAAAATTCAG	ATTANATGCT	TGGCTTAGAA	GAATGCAAAG	300
CTTCACTGAG	CCTAATAATA	TGGATCCCAG	TGGGTGAGTG	GAGGTGAGTT	CACTCGAG	358

## (2) INFORMATION FOR SEQ ID NO:436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GCTCGAGAGA	GCTTTTTTTT	TTTTTTTAA	ACATTGTATC	ATTAATTTAT	CACGTGTATC	60
CAAGCTCCTT	TGAGTTTCCC	TGCCCCATC	CCTGTGTCAT	TCCAGCCATA	TCCAGCTACT	120
CCTTCCATGC	TTCCCCATT	CTTGTTCTG	ACTCTATTAC	TCCCAGTCCA	AATCTTGCTC	180
TTCACGTCT	GCACCTGTG	CTCTCCTCT	TCTCAAAAA	TCTACCCAAA	TTCCACCCCT	240
CTTCACAGGC	CCCTCGAG					258

## (2) INFORMATION FOR SEQ ID NO:437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

CAAGCCGCGC	ATATTAGAGA	GATGGAAATA	AAGCTTCCTT	AATGTGTAT	ATGTCTTTGA	60
AGTACATCCG	TGCATTTTTT	TTTAGCATCC	AACCATTCC	CCCTTGAGT	TCTCGCCCCC	120
TCAAATCACC	CTCTCCCGTA	GCCCACCGA	CTAACATCTC	AGTCTCTGAA	AATGCACAGA	180
GATGCCTGGC	TACCTCGCCC	TGCCTTCAGC	CTCACGGGGC	TCAGTCTCTT	TTTCTCTTTG	240
GTGCCACCAG	GACGGAGCAT	GGAGGTCACA	GTACCTGCCA	CCCTCAACGT	CCACTCGAG	299

## (2) INFORMATION FOR SEQ ID NO:438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GAATTCCTAC	TAAATAATAT	TAAGCAGGAA	TTTTTTAGGT	GTGCTTTTTT	AGCTCCTTTT	60
TATCAGTTCT	GGGAAGCAAA	CAGTGCTGCA	TCTCCTTTGC	TCTCATAGAA	TTCTGTAATT	120
TTTATACCAC	AGGTCTCTGC	TAAAAGGCGG	CATGTGTTTA	GAAATTCTAA	AAATGAGGGC	180
TCTGAACCTT	GTAAGTGTCC	TGATACGTTT	TCCCTTTTTT	AATCCCAACC	CCCTCGAG	238

## (2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```
GAATTCGGCC TTCATGGCCT ACAACTTGCA CTTGCTCCA GCATCACTGG CCTCCTGCTG      60
TTATTTAGGT ATACTAGGCA TTTCTGTTT TAGGGCCTTT GTACCTCCAG TTCCCTCTGT      120
TTGGAATGCT TTTCCCAGA TAGCCCTGTG GTTAAATCTC TTACTTCCTT TGGGTCTGTG      180
CTCAGATGTT ACTTCTCAG AGGGTCCCCC AAGCCCCCAT GCACTCGAG      229
```

## (2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```
GAATTCGGCC TTCATGGCCT AGAGTCTATT AACTATTTT CTGTTATACC CTGCCAGAAA      60
AGAATTTTAA AAGTTAGTTT ATGTTTGTG TAACCATGTT CTTCAGAATG CAGGTATGTG      120
AGCATCATGG TTTCTGGGTA ATTCTGCTGC TCCTGCTTT GAAAATGGAG ATACCACTTG      180
CAGCTTATCC CACTGCTGAG TATTCCAGCA TTGGTAGTGG TTTCACTCCA TTGCATCCAT      240
CCAGAACTTT CACACAGGCC TCCCATTAC CCAGCATCCT CGAG      284
```

## (2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```
GAATTCGGCC TTCATGGCCT AATAAAATAA AAATTGGAAG AATGGCATTT TATTACAGTA      60
TAGTTAAGAG ATTGGCTAAG GCAGTAAATA AAACCTAGAA ATGCTCAAAT TTATTGTAAA      120
TTGCTTTTAT AATCATTGAT ATATAAGCA TGCTACTGCT AATCAATTAG TTTTATGTAT      180
TAAGACCTAT CAGCATGTCT TTTTTTAGT ATCTGGTTGA CTAAACATG ATGTTCTCTG      240
TACCATTTAA CATTTTCAAG ACATATTCTC CCCAACTCG AG      282
```

## (2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 241 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```
GAATTCGGCC TTCATGGCCT ACTCACCTGC AATCTATTGT TTATATTGTT GCTATGTATC   60
TCTATTCTTT CTGCATCAAA TAATGAATAG CTCATTTTGT GTTGCCCTCA AGTATGACAA   120
ATTCCCTTCC AAATGTGATT CCAGACAGTA TATCCAAACA TGTCTTTCTT TTCCCAATTCC   180
TGATCATCCT ACATGTCAAG CACTGCCAAC GTTTACTCAA GAAAGCTTGG TTAGAACCCA   240
G                                     241
```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (E) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

```
GCAAGCACAA ATCTAACCAT GAGCTTCAGC AATCAGCTCA ATACAGTGCA CAATCAGGCC   60
AGTGTTCCTAG CTTCAGTTC TACTGCAGCA GCTGCTACTC TTTCTCTGGC TAATTCAGAT   120
GTCTCACTAC TAAACTACCA GTCAGCTTTG TACCCATCAT CTGCTGCACC AGTTCCTGGA   180
GTGCCCAGC AGGGTGTTTC CTGCGAGCCT GGAACCACCC AGATTGCAC TCAGACAGAT   240
CCTCTCGAG                                     249
```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

```
GAATTCGGCC TTCATGGCCT AGGGATTTTT TTTCTTTTTT TTCCTCATAT GTGAAGTAAT   60
AGTCTCTTCA CAACAGAAGA AGCCACAAAA CTAAACTTAT TGGTCACTGA ATTTCTTCA   120
AGGTACGTA CCTCTTGGT ATTTTAAATC TAGATTATGT TGATTTTAT ATTTTGTTC   180
TCATTTTCT ATTTCTTGT TTTCTTACT GCAAATGGC TCGAG                                     225
```

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

```

GAATTCGGCC TTCATGGCCT AGTTTTGGAG AGCTCTACCT ACTAGCTGGT TATTTCTTAC      60
ATTAAATTAA TACCTTTAAA AAGTATTATG AAAATAACAC ACTCAGTAAA AGAAATTTTA      120
AAAAACAAAT GCAATAAAAA TGTGTTTCTT TTCAACCTTT GACTTGTCAC TTCCTCCAGC      180
TTTTCCCTTA TTAACTGTG AGAGGTATTC TCTATTAGCA GTTACTTATC CCCTTCCTCA      240
AACTCGAG                                         248

```

## (2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

GGATTGAATT CTAGACCTGC CTCGAGCGAC CTCTAGAATC CTACATTTGA AATATTCTGG      60
CAGTGAGGTG TTCATCCTAA CTCAGTCAGG TAGCTGTGGA CAGCCTTCAC CTGTTAGGAG      120
CTCCTTAGAA ATAAATTCTG AATACCTTTG GTTTTCTTTT ATCCTCCAGA GGAATTTCCA      180
CTATCTCCGA AGCTGTCCT TGTCCACTG ACAATTCGCT TAGTTAATGT TCTTTTTCAG      240
CCTGTACTAT CTCGAG                                         256

```

## (2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

GAAGGCAAGA AAATCTATGG AAAGAGAAGG CTACGAGTCC TCGGGCAATG ATGACTACAG      60
GGGTAGTTAC AACACCGTGC TCTCAGGCC TTTATTGAA AAGCAGGACA GAGAAGGTCC      120
AGCCTCCACG GGAAGCAAAC TCACCATTCA GGAACATCTG TACCCCGCGC CTTTCATCACC      180
TGAGAAAGAA CAGCTGCTGG ACCGCAGACC CACTGAATGT ATGATGTCGC GATCAGTAGA      240
TCACCTCGAG                                         250

```

## (2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

GAATTCGGCC TTCATGGCCT AGCTGGGGGG AATAGTTTAT GTGATAAGGA GTCAGTCGGA      60
CAGAGTGGGG TGAAAGATGT TCAGACAGGG AAACACACAT GCAANAGAGG GAAGGTGGGA      120
CACAGCATAT GCNTCCAACA TTTGGTAGGG CCGAGGCCCC ACATGGGAGC AGTGAGAGGT      180
TAGGGATCGA CGCTCGAG                                         198

```

## (2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```
GAATTTTCCT TACCAGGAAA ATTCATGCTT TACAATTTGT CAGAGGTGCA CATTACTAAT      60
TACAATAGGT CACACTTTTT CTATGCGCTT CATTATAATA TTGGCAACTT TATTATGCCC      120
CATTACATAC TGTATTATGC TCTTACTTTA TATGCATTTT GAG                          163
```

## (2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```
GAATTGCTGA TATCTTATAA AGGGGACCTT TTTTCTTTAC ATTTCTGACG GTTTTATCA      60
GAATGTATGT ATTAATGCTA TTTGTCTTTG TATATTTATT TTATTTCCAG CCACCTCTCG      120
AG                                  122
```

## (2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```
GAATTCGGCC TTCATAGCCT AACTCAAGAT CTCCCATCTA TTAAAGCAGA GGAATAACTT      60
TTGTAGGCTT AATACTGCTT TCTCACTTAG GAAAAGTTGA AATTAAGAAC ACACAGGAAG      120
GGATCATTTT CTAAGGTTTA TGTCTCAAC ATCAAATTGA GTTGAAACTT GACTACAGGC      180
CATCTGCTCA TTCAAAGCAT TACAATAAAT CTGTCCTATT GATGATCAAA ATGAGAGCTG      240
AATTGGATGC AGGATTGGAC ATTGCAAGCT GTTCTCCCAA GTGGGATGGA AAGGTGCTCG      300
AG                                  302
```

## (2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```
GAATTCGGCC TTCATGGCCT ACAAAAATAT TTATTGACT GAATGATTTA ATATGCAGTT    60
ATGGTGTTTA ATATATCATG TGTTATTGTG TTGTTTAAAT ACAGACATAA CCCACAGTTA    120
TCTTGAACAA GAAACTACGG GGATAAATAA AAGTACGCAG CCAGATGAGC AACTGACTAT    180
GAATTCTGAG AAAAGTATGC ATCGGAAATC CACTGAATTA GTTAATGAAA TAACATGTGA    240
GAACACAGAA TGGCCCGGAC TCGAG                                           265
```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```
GAATTCGGCC TTCATGGCCT ACTTTAATTT CTCTGAGCAG TATTTTACAG TTTTGATGTA    60
TAAACCTGGC ACAGATTATG TTCAGTTTAT TTCTAAGTTT AAGTCATGTT TTTGAATGTT    120
ATATTAAAGG ATATTTTCTT TTTTAAAAAA TCTACAATGT TTATTTTATT ATTATTATTT    180
TTAATCTCGC TTCATACCA AGGCTGGAGT AAAGTGACGC GACCTCAGCT CGAG           234
```

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

```
GAATTCGGCC TTCATGGCCT ACGCACATCC GCAGTCAGCC ACCTCGCGCG CGCCTCCAGG    60
AGCAAGGATG GAGAGGCTGG TGATCAGGAT GCCCTTCTGT CATCTGTCTA CCTACAGCCT    120
GGTTTGGGTC ATGGCAGCAG TGGTGCTGTG CACAGCACAA GTGCAAGTGG TGACCCAGGA    180
TGAAAGAGAG CAGCTGTACA CACCTGCTTC CTTAAATGTC TCTCTGCAA ATGCCCAGGA    240
AGCCCTCATT GTGACATGGC AGAAAAAGAA AGCTGTAAGC CCAGAAAACA TGGTCACCTT    300
CAGCGAGAAC CATGGGGTGG TGATCCAGCC TGCCTATAAG GACAAGATAA ACATTACCCA    360
GCTGGGACTC CAAAACTCAA CCCTCGAG                                           388
```

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

```

GAATTCGGCC TTCATGGCCT AGCTGATATT ATTCTGAGT TTTTGCTTAT TTGCTTTCTA    60
CATAGAATCA ATAAATTTGA CAACTAGCAT TGCCTATATA TGCAGGTGTG ATACTATTCA    120
GGGTACTAGT ATATTGGCCA CTCATTATGA AACTTTCAGG TCCTCATATA TTTTCTTTTA    180
TTACAATGAT CTACTTATTT CTGATAAATA TTGGATTCAT AGAGGCTAAA GGGCTGGGAA    240
AGGAAAACAT TCGTGACTAC TTACAACCAT TTGATACGAG TTGTGTCAAT ACAGACCTCA    300
CACAGCAGCA CCTCGAG                                                    317

```

## (2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```

GAATTCGGCC TTCATGGCCC ACAAATGGT AATACAAATA AACCCTACT TACTGCTTTT    60
AATGTTAGTT TGTTTTTTTT TTTTGTAGAC AGAGTCTCGC TGTGTCGCCC AGGCTGGAGT    120
GCAGTGGCGC GATCTTGGCT CACTGCAAGC TCCGCCTTTC GGGTTCACAC CATTTTCCTG    180
CCTCAGCCTC CCGAGTAGCT GGGACTGCAG GCGCCCGACT CCGGGTTCA CACCATTTCTC    240
CTCCCTCAGA CTCGAG                                                    256

```

## (2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

GAATTCGGCC TTCATGGCCT AGGAGAATCG TGAGACCTCT ATTTCATAT CTTTTCTAC    60
TACTGGAATT TTTATTTTTA CCATACCCAT AAATTACTTT CTATTTTAAG AAGCAAATAT    120
ATAATTCCTC AGTTTAGTAA AAAGTTCTCA CTTGAAAAGC TGGTATATGA ACTTTAGAGG    180
GCAGATTAAT CAACTGCTAA ATATTATTAA TCCTTCTTCT TGGAACCTTC CAACACAAAA    240
GACAGTTTAT AGAAAACAAA GTCAGTGTTT AAAACAGCTG AATGAACAT CTTTGTATAT    300
TTTATTTGTT TTTGTTTGT TTTGTTTGT TGAGACAGAG TCTTGCTCTG TTGTCCAGGC    360
TGGAGAGTAA TGGCAGATG ACTGCAACCT CTGCCTCCCG GGCTCAAGTG ATTCTCCTGC    420
CTCAGTCTCT CGAG                                                    434

```

## (2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

GAATTCGGCT TCATGGACGA GGAGATCGTG TCCGAGAAGC AAGCCGAGGA GAGCCACCGG    60

```

CAAGACAGCG CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAATC	120
TGGCTCTTCA AGCACCGCCG GGCCCGCTTC CTGCACGAAA CCGGCCTGGC TATGATTTAT	180
GGTCTTTTGG TGGGCCTTGT GCTTCGGTAT GGCATTTCATG TTCCGAGTGA TGTAAATAAT	240
GTGACCCCTGA GCTGTGAAGT GCAGTCAAGT CCAACTACCT TACTGGTAAA TGTAGTGA	300
AAATTTTATG AGTATATGCT GAAAGGAGAG ATACTCGAG	339

## (2) INFORMATION FOR SEQ ID NO:459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GAATTCGGCC TTCATGGCCT ACTTATTTT GTTCTGTGT GTTTGTTTA AATGTGTGTG	60
CGCTCATGTG AGTTTGAAGG GAGTTAGATG CAACAGCAGG AGCTGTGCTC AGGGCAGTGG	120
TGTTAATTAT GGAGGGCGTG GGAAGGGCTG GGAAGAGGAG GGGGTTGTAA GACTCCCTT	180
TTCCCTCGCA TGTAAACAGA TGCTGGTGAC TGAAAGTCTG TCTCGGTTA TGGCAAGAG	240
TGACGGAAG CTCGAG	256

## (2) INFORMATION FOR SEQ ID NO:460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GAATTCGGCC TTCATGGCCT AATTGAAAA TTCATAAGTT TCTACCAATA CTTCCAATT	60
CAATCCAACA TCTGAGGATC TCCCTAGATT TCCTATTTC ATGATTATAA CTCTGTACC	120
AGATGATAAG AAACATGGAT CTGACTATAC TCAATTTATT CACATATTTT CTCAGTGAAC	180
TAACTTATTT GCTGAATATA ACCAGTCCCC AGCCTTCCAA CTGCCTCTCT CACTTGCCAC	240
CTCTGCATCT TCCCCCACTG TCTTCCTCAG CAATCAGACT GCCTCTTGCC AAGTCATCAC	300
CACAGCACCC CACTCTCGAG	320

## (2) INFORMATION FOR SEQ ID NO:461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GAATTCGGCC TTCATGGCCT ACCCTCTACT ATTTTGAAC CAAATCAACA ACAACCTATT	60
TAGCTGTTC CCAACCTTTT CCTCCGACCC CTAACAACC CCCCTCCTAA TACTAACTAC	120
CTGACTCCTA CCCCTCACA TCATGGCAAG CCAACGCCAC TTATCCAGTG AACCACTATC	180
ACGAAAAAAA CTCTACCTCT CTATACTAAT CTCCTACAA ATCTCCTTAA TTATAACATT	240

CACAGCCACA GAACTAATCA TATTTTATAT CTCTTCGAA ACCACACTTA TCCCCACCCA 300  
TCTCGAG 307

## (2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GAATTCGGCC TTCATGGCCT AGTACAATTT AATATAATTT CTTACAAGTT TATTACCTAA 60  
 AACTTTGCAA ATAATTGAAG TTAGAAGCTT TGGATTTTGT TTTTAGAGCT TAATCCTTTT 120  
 CTGTAAGTGG AAATCCTTTC CACTGGTTTA TTTTCCTTTT GATTTTATTT TACTTTGACA 180  
 CCCTAAAGGT TTAGTGTTCC TGTTTTTAAA TCTACTGATC GTTCTTATG AGATTCCTTA 240  
 GAGTACCCCT CGAG 254

## (2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 283 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GAATTCTAGA CCTGCCTCGA GAGGACGCCG GAGAGAAATG AGTAGCAACA AAGAGCAGCG 60  
 GTCAGCAGTG TTCGTGATCC TCTTTGCCCT CATCACCATC CTCATCCTCT ACAGCTCCAA 120  
 CAGTGCCAAT GAGGTCTTCC ATTACGGCTC CCTGCGGGGC CGTAGCCGCC GACCTGTCAA 180  
 CCTCAAGAAG TGGAGCATCA CTGACGGCTA TGTCCTCCATT CTCGGCAACA AGGTAGCGCA 240  
 GCTGCTTTGG GGAGCTCCTC CCTACTGCCC AGCAAACTC GAG 283

## (2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GAATTCGGCC TTCATGGCCT AAAAAGTGGT TCCTATTTTC CTGGTTGAAC CTTGAGTGAT 60  
 ACACCCAGTA TTGTACCACC CAATTAGTAG ACATTATTTT TCCTTAGGTC ATATTATTCT 120  
 CAGCTTATAG AGCAAGAAGT TGAAGCTTAA AGGGTTAGAT TACTTGCCCA AGGTAATACA 180  
 GCAAGAATCT TATTTTCATCC AACCTAGAGT GAATATTTCC CCCACATCTC GAG 233

## (2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

```

GAATTCGGCC TTCATGGCCT ACTGATGTTG AAGACGACAC CACGGCTTTG ATGGAATATC      60
AGATATTGAA AATGTCCTCT TGCCTGTTCA TCCTTCTGTT TCTCACACCT GGTATTTTAT      120
GCATTTGTCC TCTCCAATGT ATATGCACAG AGAGGCACAG GCATGTGGAC TGTTCAGGCA      180
GAAACTTGTC TACATTACCA TCTGGACTGC AAGAGAATAT TATACATTTA AACCTGTCTT      240
ATAACCACTT TACTGATCTG CATAACCACT TAACCCAATA TACCAATCTG AGGACCCTGG      300
ACATTTCAAA CAACAGGCTT GAAAGCCTGC CTGCTCACTT ACCTCGGTCT CTGTGGAACA      360
TGCTGTCTGC TAACAACAAC ATTAACTTC TTGACAAATC TGATACTGCT TATCAGTGGA      420
ATCTTAAATA TCTGGATGTT TCTAAGAACA TGCTGGAAAA GTTTGTCTCT ATTAATAATA      480
CACTAAGAAG TCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```

GAATTCGGCC TTCATGGCCT AGCCCCGACT AGCTTTGCCC TAACTCCTTC ATCAAAAGAC      60
CCCCCGCCAG CTTCCACAC CTCATACGCA GCCACATCTG CCCTATTCTC CATGCTTTCC      120
AGCTTGCCCTG CCCTTCCTCA TCTCTCCCTG CCGTGCAGA CCTCCACCCT TCTTTCCTCC      180
ACCCCTCCAT CCCCCAATGC TTGTAGACCT TCCATTCACT CCGTCTCATC GTGCGTGGTC      240
TCTGATCGTC CATCACCTGA CCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```

GTTTACATAA ATATTATACT AGCATTTACC ATCTCACTTC TAGGAATACT AGTATATCGC      60
TCACACCTCA TATCCTCCCT ACTATGCCTA GAAGGAATAA TACTATCGCT GTTCATTATA      120
GCTACTCTCA TAACCTCAA CACCACTCG AG

```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

CAATATTTCA AGCTATACCA AGCATACAAT CAACTCCAAG CTCGGAATTT TAACTTCATG	60
GCAAACAGAA AAGCTAGACT GAGTTATCAG TGTTGTGAGA GGAATATTTG GCCCAACAAG	120
AGTTGTTGGG GTGGGAGGAG GGAGAGACAA AAGGAAAGGA CTGCCAGCTC TCAGAGGGTG	180
GAGATGGGGG ACCTCGAG	198

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC TTCATGGCCT ACTGCTATAT TCAAGTTTCT CCCACTACTG TGGTTTCTTT	60
TTTTTTTTTT TTTTTTTTTT TTTTGAGACA GGGTCTTGCT CTGTCACCCA GGCTGGGGTG	120
CAGTGGTGCG ATCTCGGCTC ACTGCAAATT ACACCTCCTG GATTGAGCA ATTCTCATGC	180
CTCAGCTTCC TGAGTAGCTG GGATAACAGG TATGCACCAC CACCCCTGGC TAATTTTGT	240
GTTTTAGTA GAGACAAGTT CTCACCATGT TGTCCAAGCC ACCTCGAG	288

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC TTCATGGCCT AAAAGAAGAA TACTAATTAG AATTGAGTT CTAGGGGTTT	60
TTCTAGGTT TTTCATTCTA GACTTAGCTT TTATTCAAAC CTGTTGATCC TGCATAGGGG	120
TAGTCTAGCT TTAATAAATA AAACAATAAA CATAAATGAG CCTATTGAGT TCAATCAGAG	180
TAGGGAGCAG TTTTATTGAA CAGCACATTT TCAAATTCCT CAGTTGTGTT TTGTTTTTCA	240
GCTACGTGTC TCTCTGTGAT AATGAAAAGA CAGGTTGCAA AGCCCGGGAA CTAAATCAG	300
TTTATGTGGA TGCAGTAGGA CTCGAG	326

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

GAATTCGGCC TTCATGGCCT AGTGTAAGT GTTTTGAC AGTGCCAGA AATTGTCAGT    60
ATTTAATGGT CCTTCCTCCT TATTTATTTT TATTACTTGT TTTTGTTTTT TTGAGACAGT    120
GTCTTGCTCT GTCGCCAGG CTGGAGAGCA GTGATATTAT CGTGACTCAC GGCAGCCTCG    180
ACCTCCCAGA CTCAGGTGAT CCTTCACCT CAGCCTCCCA GGCAGCTGGG ACCATAGCTA    240
TGAACAAACA CGTCCAGCTA TGTTTTGTAT TTTTGTGAA GACGGAGTCT CACCATGTTG    300
CCCAGGCTGA TCTCCAACTC CTCGAG                                     326

```

## (2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```

GGAAAGGTGT TGTCCCTTGT AACATTTTGG TTGGCTATAA AGCTGTATAT CGTTTGTGCT    60
TTGGTTTGGC TATGTTCTAT CTTCCTCTCT CTTTACTAAT GATCAAAGTG AAGAGTAGCA    120
GTGATCCTAG AGCTGCAGTG CACAATGGAT TTTGGTTCTT TAAATTTGCT GCAGCAATTG    180
CAATTATTAT TGGGGCATTG TTCATTCCAG AAGGAACCTT TACAACGTGT TGGTTTATG    240
TAGGCAACCT CGAG                                     254

```

## (2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

GAATTCGGCC TTCATGGCCT ACAGAAATCT AATTCCTGGT GCTATTTGCA ACTACATATA    60
TTTAAATAC AAGGAGATAA ATACCCAGAA CACATTAAGC CTACTGATTT AAACAGAACAA    120
TTTCAAGACT GCTACACAGA AAGGGAAGGA AGCTGTTAAC CCAGCACAGC AGCACACCTC    180
ACATATTTAC GTCTCAGAGA TTAAATGGAA AGAAAGGATC AATCAAAACC TTTAATGCTC    240
AGTTTTCACA AACACAGTCA AGTCTATCAA ATTTCCAGAT TTACAG                                     286

```

## (2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

GAATTCGGCC TTCATGGCCT ACAATTAAAA GGTTCGTGTA AATTACGTCT TTCAGTCTGA    60
AATTACTCTG AGAATTFACT TAAAATTTT CCATTTAAAA ACAGGTATAA AATTAATTGC    120
TAGTTTCCAT AATCACCAG TATAAAGATA GAAAAGACCT GTAAGACAAC TGTGTGGTTA    180

```

AATACATGAT AACACATTTA CGTGCCTTTT ATAGAAATCC ACTTATTATG TACATACTGG	240
CTTGTTTTTTT TTCCCACTTC TCCAGTACAC TATTTTCAGGC ACAGGCTCAA AATTTGAACC	300
CAAATGGTCT GTTAGGTCTC TTGACTTTTT CAGTTCAAAG CTCTGCTAAT CTGCTAAACC	360
TAGCCCCAAA CCCACTCGAG	380

## (2) INFORMATION FOR SEQ ID NO:475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GAATTCTAGA CCTGCCCGGA GCCCTGACCT AGTCCGGCGT GGAGAGAGGA ATGGAAGCA	60
GTGTCCCTTT TGAGAAGGCA AATTTACAGC TGGCTTTTGT AATCCTAGCT ATTTTTTGT	120
TGTTTGCTAA GTCTTTGATA GTCCCCAGTG TGGTTTGTCT GCCAGTGATC TCAGCACCAC	180
CAGAGAGCTT GTTAGAAATG CGGCATCCCA ACCCCACCAC AGCCCTCCA AGTCAGATAC	240
TCCCCCTCT CGAG	254

## (2) INFORMATION FOR SEQ ID NO:476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GAATTCGCTG TGGAGCTGGG CGTGCTGTTT GTCCGGCCCC GGCCCGGAAC CGGGCTGGGT	60
AGAGTGATGC GGACCCCTCCT GCTGGTGCTG TGGCTGGCGA CGCGCGGAAG CGCGCTCTAC	120
TTTCACATCG GAGAGACGGA GAAGAAGTGC TTTATTGAGG AGATCCCGGA CGAGACCATG	180
GTCATAGGAA ACTACCGGAC GCAGCTGTAT GACAAGCAGC GGGAGGAGTA CCAGCCGGCC	240
ACCCCGGGGC TTGGCATGTT TGTGGAGGTG AAGGACCCAG AGGACAAGGT CATCCTGGCC	300
CGGCAGTATG GTTCCGAGGG CAGGTTCACT TTCANTTCCC ATACCCNTGT GTGAGCACCA	360
GATCTGTTTT CANTCCAATT CCACTCGAG	389

## (2) INFORMATION FOR SEQ ID NO:477:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAATTCGGCC TTCATGGCCT AGAAGGAAAT AAAGGCCCCG ATTTCTGGAG TTCTGAGCCT	60
ACTTTTTTTG GGTGCATTTT GAAACATACG GATTTTACCG CTAGTATATT CAGTGAGGAA	120
GGAAGGCTTC TGAAGGATTG ATGATCCCCA AACTGGATTA TGTGTTTCATG ATAATGGTGT	180
ATTTGTTGGC CTAGCATAGT GAGGTGAGGT AGGTCTTTAA AATGGCTCAT TATAACATC	240



ATTGTTCTCTG AGCTCACTTG CCCTTGCCATC TCCTGCCAGA GTGCTTTGTA CATAGTAGGC	300
CCTCATCAAT GCTTGTAGAT TTAAATTTCG GAGGCACACT TGGAAGACAA TGGTGGCTGG	360
TAAATTAAAT ATCAGGGTTA GCAACTTCAT TTCTGCTNAC GCTTAAAAAG TGCTGCGCGA	420
GGAAACTCGA G	431

## (2) INFORMATION FOR SEQ ID NO:478:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GCCTCTGNTT TTAATTCATT GGCAACTGTT ACGATGGAAG ACCTGATTCG ACCTTGTTTC	60
CCTGAGTTCT CTGAAGCCCG GGCCATCATG CTTTCCAGAG GCCTTGCCCTT TGGCTATGGG	120
CTGCTTTGTC TAGGAATGGC CTATATTTC TCCCAGATGG GACCTGTGCT GCAGGCAGCA	180
ATCAGCATCT TTGGCATGGT TGGGGGACCG CTGCTGGGAC TCTTCTGCCT TGGAAATGTT	240
TTTCCATGTG CTAACCTCC TGGTGCTGTT GTGGGCTGT TGGCTGGCT CGTCATGGCC	300
TTCTGGATTG GCATCGGAG CATCGTGACC AGCATGGCT TCAGCATGCC ACCCTCTCCC	360
TCTAATGGGT CCAGCTTCTC CCTGCCCACC AATCTAACCG TTGCCACTGT GACCACACTT	420
CTCGAG	426

## (2) INFORMATION FOR SEQ ID NO:479:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAATTCGGCC TTCATGGCCT AAATTTTCAG GCAGTTTGAA GTATCTGGCA GAAAAAGTAA	60
ATTGAAATCA TTGGGACGTT GATTTTAA TACCTAGAA GCAATCCCAA TGCTTTATGT	120
AATACTAAAA TTTCTCCTCT CTCCTTTCTT TATCTCTCTC TCCCCTGAAA ATAATCATT	180
TTTTTCCAGT GCCAGTTCAG ATCTTGGCAA CAGTTGTTT GAAAAAGTAC CTGAACAAAA	240
TACATTTTAT AAAGTAAAGT ATTCAGGAAC TGACAGAACT GGAGAAGAAT ATATTTATGT	300
TACAGAAGTC ATGACAACC TCGAG	325

## (2) INFORMATION FOR SEQ ID NO:480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GGCAAGTAAC AGGTTGCAAG AATTGGAGGC AGAGCAACAG CAGATCCAAG AAGAAAGAGA	60
ATTACTGTCC AGACAAAAGG AAGCTATGAA AGCAGAGGCA GGCCAGTTG AACACAATT	120

```

ACTACAGGAG ACAGACAAAT TAATGAAGGA AAAACTAGAA GTACAATGTC AAGCTGAAAA    180
AGTACGTGAT GACCTTCAAA AACAAAGTGAA AGCTCTAGAA ATAGATGTGG AAGAACAAGT    240
CAGTAGGTTT ATAGAGCTGG AACAAAGAAAA AAATACTGAA CTAATGGATT TAAGACAGCA    300
AAACCAAGCA TTGGAAAAGC AGTTAGAAAA AATGAGAAAA TTTTATAGATG AGCAAGCCAT    360
TGACAGAGAA CATGAGAGAG ATGTATTCCA ACAGGAAATA CTCGAG                    406

```

## (2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

```

GAATTCGGCC AAAGAGGCCT AGTCGGTGCC TCATTGGTAT AAATGTTATG TCTGCATGGG    60
TTTTTCTAC AATTCTTTC TAAGATTATT TCTCCCCAAA GCTCAGCACT TTGGAATTT    120
TTCATTCTCA TCCAAAAATG GAAGCAATTT TATGTAAATG TCTCTTGAA GCAGTGTGG    180
AATTCATATT TTGGGTAGCA GAAGCAGTAG TTACAAGGT AGTGGTGTCT TTTGTGGTGG    240
TGGTGGCACC TGCTGCAGTT GTTCATATTT GGGGTGCAGG AGTAGGGAGG GTAGGATCAG    300
TTGAGAATT TACAGGAAA AATGGAGGTC CAGGTGGATA GGGTCTAGAA TTCAATC      357

```

## (2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

```

GAATTCGGCC AAAGAGGCCT AAGTGACTCC AGAGCCTCCT GCAAGATGCT GTTGATTCTG    60
CTGTCACTGG CCTTGCTGGC CCTGAGCTCA GCTCAGAACT TAAATGAAGA TGTGAGCCAG    120
GAAGAATCTC CCTCCCTAAT AGCAGGAAAT CCACAAGGAG CACCCCCACA AGGAGGCAAC    180
AAACCTCAAG GTCCCCATC TCCTCCAGGA AAGCCACAAG GACCACCCC ACAAGGAGGC    240
AACCAGCCTC AAGGTCCCC ACCTCCTCCA GGAAAACCA AAGGACCACC CCTATTCTC      303
GAG

```

## (2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

GAATTCGGCC AAAGAGGCCT AAGCAGACAC AATGGTAAGA ATGGTGCTG TCCTGCTGTC    60
TCTGCTGCTG CTTCTGGGTC CTGCTGTCCC CCAGGAGAAC CAAGATGGTC GTTACTCTCT    120
GACCTATATC TACACTGGGC TGTCCAAGCA TGTGAAGAC GTCCCGCGT TTCAGGCCCT      180

```

TGGCTCACTC AATGACCTCC AGTTCCTTTAG ATACAACAGT AAAGACAGGA AGTCTCAGCC	240
CATGGGACTC TGGAGACAGG TGGGAAGGAAT GGAGGATTGG AAGCAGGACA GCCAACTTCA	300
GAAGGCCAGG GAGGACATCT TTATGGAGAC CCTGAAAGAC ATCGTGGAGT ATTACAACGA	360
CAGTAACGGG TCTCACGTAT TGCAGGGAAG GTTTGTTGT GAGATCGAGA ATAACAGAAG	420
CAGCGGAGCA TTCTGGAAAT ATTACTATGA TGGAAAGGAC AAACCTCGAG	469

## (2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GAATTCGGCC AAAGAGGCCT ACTACTTCTG TAGTCTCATC TTGAGTAAAA GAGAACCCAG	60
CCAACTATGA AGTTCCTTGT CTTTGCCTTC ATCTTGGCTC TCATGGTTTC CATGATTGGA	120
GCTGATTCAT CTGAAGAGTA TGGGTATGGC CCTTATCAGC CAGTTCAGG ACAACCACTA	180
TACCCACAAC CATACCAACC ACAATACCAA CCTGCCTCAA GGTCTCCAC CTCCTCCAGG	240
AAAGCCACAA GGACCACCCC CACAAGGAGG CAACAAACCT CAAGGTCCCC CACCTCCAGG	300
AAAGCCACAA CGACCACCCC CACAAGGAGG CAGCAAGTCC CGAAGTTCTC GATCTCCTCC	360
AGGAAAGCCA CAAGGACCAC CCCCAAGAGG AGGCAACAAA CCTCAAGGTC CCCACCTCC	420
AGGAAAGCCA CAAGGACCAC CCCCAAGAGG AGGCAGCAAG TCCCGAAGTG CCGATCTCC	480
TCCAGGAAAG CCACAAGGAC CATCCACAA CTCGAG	516

## (2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GAATTCGGCC AAAGAGGCCT ACTTCACTTC AGCTTCACTG ACTTCTTGAC TCTCCTCTTG	60
AGTAAAAGGA CTCAGCCAAC TATGAAGTTT TTTGTCTTTG CTTTAGTCTT GGCTCTCATG	120
ATTTCCATGA TTAGCGCTGA TTCACATGAA AAGAGACATC ATGGGTATAG AAGAAAATTC	180
CATGAAAAGC ATCAITCACA TCGAGAATTT CCATTTTATG GGGACTGTGG ATCAAATTAT	240
CTATATGACA ATTGATATCC TTAGTAATCA TGGGGCATGA TTATAGAGGT TTGACTGGCA	300
AATTCACTTT TACTCATTTA TTCTCATTCA TCACACCGCA AGTCTAGGCC TCTCGAG	357

## (2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 643 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486: